



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 108250

TO: Elizabeth Kemmerer

Location: cm1/10b17/10d19

Art Unit: 1646

Sunday, November 16, 2003

Case Serial Number: 08/741095

From: Toby Port

Location: Biotech-Chem Library

CM1-6A04

Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Kemmerer,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port

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W096/34095


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Db      181 HOTKCSMLVTKAGAGSSSHWMMWFLSGSLVIVYVSTGGLIICVRRKPRGDVVKIVIS 240
Qy      241 VORKROEAGEATVIEALQAPPDVTVAVEETIPSTGSPNH 283
Db      241 VORKROEAGEATVIEALQAPPDVTVAVEETIPSTGSPNH 283

RESULT 2
US-09-934-289A-13
; Sequence 13, Application US/09934289A
; Patent No. US20020132297A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: M81098-061C1C1(M)
; CURRENT APPLICATION NUMBER: US/09/934,289A
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/342,767
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/146,950
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: (1)...(38)
US-09-934-289A-13

Query Match      100.0%; Score 1578; DB 10; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.7e-126;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MEBPGWGPMPWRSTPRTDVLRLVLYLTFGLGAPCYAPALPSCKEDEYVPGSECCPKCSFG 60
Db      1 MEBPGWGPMPWRSTPRTDVLRLVLYLTFGLGAPCYAPALPSCKEDEYVPGSECCPKCSFG 60
Qy      61 YRKEACGELTGVCPCPGTYIAHLNGLSKLQOCMDPAMGLRASNCSRTENAVCG 120
Db      61 YRKEACGELTGVCPCPGTYIAHLNGLSKLQOCMDPAMGLRASNCSRTENAVCG 120
Qy      121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
Db      121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
Qy      121 CSFGHCTIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
Db      121 CSFGHCTIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
Qy      181 HOTKCSMLVTKAGAGTSSSHWMMWFLSGSLVIVYVSTGGLIICVRRKPRGDVVKIVIS 240
Db      181 HOTKCSMLVTKAGAGTSSSHWMMWFLSGSLVIVYVSTGGLIICVRRKPRGDVVKIVIS 240
Qy      241 VORKROEAGEATVIEALQAPPDVTVAVEETIPSTGSPNH 283
Db      241 VORKROEAGEATVIEALQAPPDVTVAVEETIPSTGSPNH 283

RESULT 3
US-09-935-727-31
; Sequence 31, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
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; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-727-31

Query Match      100.0%; Score 1578; DB 10; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.7e-126;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MEBPGWGPMPWRSTPRTDVLRLVLYLTFGLGAPCYAPALPSCKEDEYVPGSECCPKCSFG 60
Db      1 MEBPGWGPMPWRSTPRTDVLRLVLYLTFGLGAPCYAPALPSCKEDEYVPGSECCPKCSFG 60
Qy      61 YRKEACGELTGVCPCPGTYIAHLNGLSKLQOCMDPAMGLRASNCSRTENAVCG 120
Db      61 YRKEACGELTGVCPCPGTYIAHLNGLSKLQOCMDPAMGLRASNCSRTENAVCG 120
Qy      121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
Db      121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
Qy      121 CSFGHCTIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
Db      121 CSFGHCTIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
Qy      181 HOTKCSMLVTKAGAGTSSSHWMMWFLSGSLVIVYVSTGGLIICVRRKPRGDVVKIVIS 240
Db      181 HOTKCSMLVTKAGAGTSSSHWMMWFLSGSLVIVYVSTGGLIICVRRKPRGDVVKIVIS 240
Qy      241 VORKROEAGEATVIEALQAPPDVTVAVEETIPSTGSPNH 283
Db      241 VORKROEAGEATVIEALQAPPDVTVAVEETIPSTGSPNH 283

RESULT 4
US-10-020-787-2
; Sequence 2, Application US/10020787
; Publication No. US20020102258A1
; GENERAL INFORMATION:
; APPLICANT: Harrop, Jeremy A.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Reddy, Manjula P.
; APPLICANT: Truneh, Alemsseged
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-Like 2 (TLR2) Antibodies
; FILE REFERENCE: GH50027C1
; CURRENT APPLICATION NUMBER: US/10/020,787
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 09/403,815
; PRIOR FILING DATE: 1999-10-26
; PRIOR APPLICATION NUMBER: PCT/US98/09744
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/046,249
```


;; PRIOR FILING DATE: 1997-05-12
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 283
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-10-020-787-2

Query Match 99.8%; Score 1575; DB 14; Length 283;
Best Local Similarity 99.6%; Pred. No. 1.4e-125;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPMRSTPRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYVSGCCPKCSPG 60
DB 1 MEPPGDMGPPPMRSTPRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYVSGCCPKCSPG 60
QY 61 YRVKACGELTGTVCEPCPGTGTIAHLNGLSKLCQCCDPMAGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCEPCPGTGTIAHLNGLSKLCQCCDPMAGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQRYVKGSTESODTLCONCPGTSPNGTLEECQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQRYVKGSTESODTLCONCPGTSPNGTLEECQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKKRKRPGDVVKYIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKKRKRPGDVVKYIVS 240
QY 241 VQRKQAEAGEATVIEALQAPPDVTYVAVEETIPSTGRSPNH 283
DB 241 VQRKQAEAGEATVIEALQAPPDVTYVAVEETIPSTGRSPNH 283

RESULT 5

US-10-066-209-2
;; Sequence 2, Application US/10066209
;; Publication No. US20020115110A1
;; GENERAL INFORMATION:
;; APPLICANT: Brigham-Burke, Michael R.
;; APPLICANT: Young, Peter R.
;; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
;; FILE REFERENCE: GH-50030-D1
;; CURRENT APPLICATION NUMBER: US/10/066, 209
;; PRIOR FILING DATE: 2001-10-25
;; PRIOR APPLICATION NUMBER: 09/072, 993
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/055, 513
;; PRIOR FILING DATE: 1997-08-13
;; PRIOR APPLICATION NUMBER: 60/056, 980
;; PRIOR FILING DATE: 1997-08-26
;; PRIOR APPLICATION NUMBER: 60/057, 550
;; PRIOR FILING DATE: 1997-08-29
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 283
;; TYPE: PRT
;; ORGANISM: HOMO SAPIENS
US-10-066-209-2

Query Match 99.6%; Score 1572; DB 14; Length 283;
Best Local Similarity 99.6%; Pred. No. 2.5e-125;
Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPMRSTPRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYVSGCCPKCSPG 60
DB 1 MEPPGDMGPPPMRSTPRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYVSGCCPKCSPG 60
QY 61 YRVKACGELTGTVCEPCPGTGTIAHLNGLSKLCQCCDPMAGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCEPCPGTGTIAHLNGLSKLCQCCDPMAGLRASRNCSTENAVCG 120

QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQRYVKGSTESODTLCONCPGTSPNGTLEECQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQRYVKGSTESODTLCONCPGTSPNGTLEECQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKKRKRPGDVVKYIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKKRKRPGDVVKYIVS 240
QY 241 VQRKQAEAGEATVIEALQAPPDVTYVAVEETIPSTGRSPNH 283
DB 241 VQRKQAEAGEATVIEALQAPPDVTYVAVEETIPSTGRSPNH 283

RESULT 6

US-09-934-289A-42
;; Sequence 42, Application US/09934289A
;; Patent No. US20020132297A1
;; GENERAL INFORMATION:
;; APPLICANT: Busfield, Samantha J.
;; TITLE OF INVENTION: NOVEL MOLECULES OF THE
;; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
;; FILE REFERENCE: MB1098-061CPCIN (M)
;; CURRENT APPLICATION NUMBER: US/09/934, 289A
;; PRIOR FILING DATE: 2001-08-21
;; PRIOR APPLICATION NUMBER: US 09/342, 767
;; PRIOR FILING DATE: 1999-06-29
;; PRIOR APPLICATION NUMBER: US 09/146, 950
;; PRIOR FILING DATE: 1998-09-03
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 42
;; LENGTH: 277
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: (1)... (38)
US-09-934-289A-42

Query Match 87.0%; Score 1373.5; DB 10; Length 277;
Best Local Similarity 93.5%; Pred. No. 1.6e-108;
Matches 245; Conservative 2; Mismatches 6; Indels 9; Gaps 1;

QY 1 MEPPGDMGPPPMRSTPRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYVSGCCPKCSPG 60
DB 1 MEPPGDMGPPPMRSTPRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYVSGCCPKCSPG 60
QY 61 YRVKACGELTGTVCEPCPGTGTIAHLNGLSKLCQCCDPMAGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCEPCPGTGTIAHLNGLSKLCQCCDPMAGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQRYVKGSTESODTLCONCPGTSPNGTLEECQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQRYVKGSTESODTLCONCPGTSPNGTLEECQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKKRKRPGDVVKYIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKKRKRPGDVVKYIVS 240
QY 241 VQRKQAEAGEATVIEALQAPP 262
DB 241 VQ-----VLTLLPLSLPP 253

RESULT 7

US-09-934-289A-44
;; Sequence 44, Application US/09934289A
;; Patent No. US20020132297A1
;; GENERAL INFORMATION:
;; APPLICANT: Busfield, Samantha J.
;; TITLE OF INVENTION: NOVEL MOLECULES OF THE

Qy	39	LPSCKEKEYVVGSECCPKSPGYRVEAGAGELGTVCPCPGYIALNLASLCLOCOM	98
Db	1	LPSCKEDEYVVGSECCPKSPGYRVEAGAGELGTVCPCPGYIALNLASLCLOCOM	60
Qy	99	CDPAMGLRASRNCSTRENAAVCGSPGHFCTVDDGHCACRAYATSPGQEVQKGTESQ	158
Db	61	CDPAMGLRASRNCSTRENAAVCGSPGHFCTVDDGHCACRAYATSPGQEVQKGTESQ	120
Qy	159	DTLCNCCPPTFSNGTLECOHQTK	184
Db	121	DTLCNCCPPTFSNGTLECOHQTK	146

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RESULT 14
US-09-934-289A-20
Sequence 20, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDI-
TITLE OF INVENTION: PROTEIN FAMILY AND US
FILE REFERENCE: MB1098-061CP1CN1 (M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 159
TYPE: PR1
ORGANISM: Homo sapiens
US-09-934-289A-20

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Query Match	53.2%	Score 839;	DB 10;	Length 159;
Best Local Similarity	98.0%;	Pred. No. 1.6e-63;		
Matches 146;	Conservative 1;	Mismatches 0;	Indels 2;	Gaps 1

QY	39	LPSCKDEYVPGSECCPKCS	PGRYVKEAGGELTGVCEPCPGTYIAHLNLSLSCLOCOM	98
Db	1	LPSCKDEYVPGSECCPKCS	PGRYVKEAGGELTGVCEPCPGTYIAHLNLSLSCLOCOM	60
QY	99	CDPAMGLRASRNRCSRTENAVCGSGPQHFCITVDDGDHCAACRAYATSSPGQVQKGTESQ		158
Db	61	CDPAMGLRASRNRCSRTENAVCGSGPQHFCITVDDGDHCAACRAYATSSPGQVQKGTESQ		120
QY	159	DTLCNCCPGTFSPNGLTLECOHQTKCSW	187	
Db	121	DTLCNCCPGTFSPNGLTLECOHQTKCSW	147	

```

RESULT 15
US-10-247-671-152
: Sequence 152, Application US/10/247671
: Publication No. US2003019472A1
: GENERAL INFORMATION:
: APPLICANT: Mikita, Thomas
: APPLICANT: Shiftman, Dov
: APPLICANT: Porter, Gordon, J.
: APPLICANT: Kaser, Matthew R.
: TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
: FILE REFERENCE: PA-0050 US
: CURRENT APPLICATION NUMBER: US/10/247,671
: CURRENT FILING DATE: 2002-09-18
: PRIOR APPLICATION NUMBER: 60/333,784
: PRIOR FILING DATE: 2001-09-19
: NUMBER OF SEQ. ID NOS: 186
: SOFTWARE: PERL Program
: SEQ ID NO 152

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: LENGTH: 277
: TYPE: PR1
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: OTHER INFORMATION: Incyte ID No. US2003019472A1 1452055CD1
US-10-247-671-152

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Query Match	17.0%;	Score 268.5;	DB 12;	Length 277;
Best Local Similarity	26.1%;	Pred. No. 6.5e-15;		
Matches	71;	Conservative	50;	Mismatches 116;
			Indels	35;
			Gaps	9

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Oy 20 VRLVLYLTFELAPCYAPAL-----PSCKEYEPAGSECCPKSPGYRVKEACCELGTV 74
Db 1 MVALPFIQCVMKG--CLLTAVHPHEPPTACKREKQYLINSCGSLCQPGKULVSDCTFEETE 58
Oy 75 CERPCEGYIAHLNGLSKLCCOMCDPMAGLRASBNSRLENAVGSSPGHFICVDGDH 134
Db 59 CLPFGSEFLDPMNRETHCHOKHYCDPMIGLRVQCKGSENDITCTEEGMHC---TSEA 115
Oy 135 CACRATVATSSPGQRYOKGTESOOTLONCPPTGFS--PNTLEECOHOTKCSW--LVTK 191
Db 116 CEECVLHSGCSGFGVKKOJATSVSTICEPCEVGFSSVSAFEEKHPMTSCERKDLVYQ 175
Oy 192 AGAGTSSSHWVWFLSGSLVIVYVCSITVGLIICVKKRRKRGDVVKVIVSVQRRQSEAGE 251
Db 176 Q-AGTKTKTVVCGPQDRLATLVVILPIIGILFA-----ILLVIVFIKKVAKKEPTNK 225
Oy 252 ATVIALQAPDV-----TIVAVEETI 273
Db 226 AP--HPKQEPQEIHPDDLPGSNTAPVQETL 255

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Search completed: November 14, 2003, 17:37:15
Job time : 31 secs

SEQ ID NO 18
LENGTH: 197
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(38)
US-09-934-289A-18

Query Match 67.2%; Score 1060; DB 10; Length 197;
Best Local Similarity 98.4%; Pred. No. 3.9e-82;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MPPGDWGPMPWRSTPRTDVLRVLVLTFLGAPCYAPALPSCKEDEYVSGECPCPKSPG 60
DB 1 MPPGDWGPMPWRSTPRTDVLRVLVLTFLGAPCYAPALPSCKEDEYVSGECPCPKSPG 60
QY 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQRYVKGSTESODTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQRYVKGSTESODTLCONCPGTFSPNGTLEECQ 180
QY 181 HQTKCSW 187
DB 181 HQTK--NW 185

RESULT 11
US-09-934-289A-30
Sequence 30, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: MB1098-061CPC1N1 (M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 30
LENGTH: 186
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(38)
US-09-934-289A-30

Query Match 67.0%; Score 1059; DB 10; Length 186;
Best Local Similarity 99.5%; Pred. No. 5.5e-82;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPPGDWGPMPWRSTPRTDVLRVLVLTFLGAPCYAPALPSCKEDEYVSGECPCPKSPG 60
DB 1 MPPGDWGPMPWRSTPRTDVLRVLVLTFLGAPCYAPALPSCKEDEYVSGECPCPKSPG 60
QY 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQRYVKGSTESODTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQRYVKGSTESODTLCONCPGTFSPNGTLEECQ 180

QY 181 HQTK 184
DB 181 HQTK 184

RESULT 12
US-09-934-289A-4
Sequence 4, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: MB1098-061CPC1N1 (M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 155
TYPE: PRT
ORGANISM: Homo sapiens
US-09-934-289A-4

Query Match 53.7%; Score 847; DB 10; Length 155;
Best Local Similarity 98.0%; Pred. No. 3.3e-64;
Matches 146; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 39 LPSCKEDEYVSGECPCPKSPGYRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCOM 98
DB 1 LPSCKEDEYVSGECPCPKSPGYRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCOM 98
QY 99 CDPAMGLRASRNCSTENAVCGSPGHFCTVODGDHCAACRAVATSSPGQRYVKGSTESQ 158
DB 61 CDPAMGLRASRNCSTENAVCGSPGHFCTVODGDHCAACRAVATSSPGQRYVKGSTESQ 120
QY 159 DTLCQNCPPGTFSPNGTLEECQHQTCSW 187
DB 121 DTLCQNCPPGTFSPNGTLEECQHQTCSW 149

RESULT 13
US-09-934-289A-32
Sequence 32, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: MB1098-061CPC1N1 (M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 148
TYPE: PRT
ORGANISM: Homo sapiens
US-09-934-289A-32

Query Match 53.4%; Score 843; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 6.9e-64;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Camelox virus (strain CP-1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=203174;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DUBAI-1992 / CP-5, and SOMALIA-1978;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87840; AAB94357.1; -
DR EMBL; U87837; AAB94354.1; -
DR HSSP; Q92956; IJMA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 349 AA; 38036 MW; EA412AE86E090E4 CRC64;

Query Match 16.8%; Score 266.5; DB 12; Length 349;
Best Local Similarity 33.1%; Pred. No. 2.1e-18;
Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

QY 21 LRLVLTFLGAPC-----YAPALPSCKEDEVPGSECCPCSPGYRVKACGEL 70
DB 1 MRSVLYSILFLSCIIINGRDVTPVAPSNCKCKDNKRNLCCLSCPGTYASRLCDSK 60
QY 71 TGTVCPCPPGTYIAHLNGLSKLQCO-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
DB 61 TMTQCTPCGSDFTFTSHNHLQACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYCYLL 118
QY 130 QGDGHCACRAVATSSPGQRYVKGSTESQDTLCQNCPPGTSPN-CTLECOHOT 183
DB 119 KSSSGCRCTISKTKGIGYV-SGYTSTDVICSRCGPGTYSHYVSTDKEPVT 172

RESULT 14
OS7103 PRELIMINARY; PRT; 348 AA.
AC 057103;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Zaire-1979;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species."
DR EMBL; U87847; AAB94364.1; -
DR HSSP; Q92956; IJMA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38184 MW; 34A5E66B27907B5 CRC64;

Query Match 16.8%; Score 265.5; DB 12; Length 348;
Best Local Similarity 32.0%; Pred. No. 2.6e-18;
Matches 56; Conservative 25; Mismatches 79; Indels 15; Gaps 5;

QY 21 LRLVLTFLGAPC-----YAPALPSCKEDEVPGSECCPCSPGYRVKACGEL 70

DB 1 MRSVLYSILFLSCIIINGRDVTPVAPSNCKCKDNKRNLCCLSCPGTYASRLCDSK 60
QY 71 TGTVCPCPPGTYIAHLNGLSKLQCO-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
DB 61 TMTQCTPCGSDFTFTSHNHLQACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYCYLL 118
QY 130 QGDGHCACRAVATSSPGQRYVKGSTESQDTLCQNCPPGTSPN-CTLECOHOT 183
DB 119 KSSSGCRCTISKTKGIGYV-SGYTSTDVICSRCGPGTYSHYVSTDKEPVT 172

RESULT 15
OS7099 PRELIMINARY; PRT; 349 AA.
AC 057099;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sierra Leone-1970;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species."
DR EMBL; U87843; AAB94360.1; -
DR HSSP; Q92956; IJMA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 349 AA; 38321 MW; FE449028CC933F57 CRC64;

Query Match 16.8%; Score 265.5; DB 12; Length 349;
Best Local Similarity 32.6%; Pred. No. 2.6e-18;
Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5;

QY 21 LRLVLTFLGAPC-----YAPALPSCKEDEVPGSECCPCSPGYRVKACGEL 70
DB 1 MRSVLYSILFLSCIIINGRDVTPVAPSNCKCKDNKRNLCCLSCPGTYASRLCDSK 60
QY 71 TGTVCPCPPGTYIAHLNGLSKLQCO-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
DB 61 TMTQCTPCGSDFTFTSHNHLQACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYCYLL 118
QY 130 QGDGHCACRAVATSSPGQRYVKGSTESQDTLCQNCPPGTSPN-CTLECOHOT 183
DB 119 KALCCRTCTISKTKGIGYV-SGYTSTDVICSRCGPGTYSHYVSTDKEPVT 172
QY 190 T 190
DB 173 T 173

Search completed: November 14, 2003, 17:31:45
Job time : 43 secs

OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Benin-1978;
RA Loparev V.N., Parsons J.M., Eposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87846; AAB94363.1; -.
DR HSSP; Q92956; IJMA.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 2.
DR SMART; SMO0208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS0050; TNFR_NGFR_2; 2.
KM Receptor.
SQ SEQUENCE 349 AA; 38308 MW; CBD2C949F994C59C CRC64;

Query Match	17.1%;	Score 269.5;	DB 12;	Length 349;
Best Local Similarity	39.6%;	Pred. No. 1e-18;		
Matches	59;	Conservative	22;	Mismatches 81;
				Indels 19;
				Gaps 5;

[illegible]

RESULT	11		
057291			
ID	057291	PRELIMINARY:	PRT, 349 AA.
AC	057291:		
DT	01-JUN-1998	(TREMBLrel. 06, Created)	
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)	
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)	
DE	Tumor necrosis factor receptor II homolog.		
DN	CRMb.		

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxId=10244;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Loparev V.N., Parsons J.M., Beposito J.J.,
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; U88144; AAB94369.1; -;
DR EMBL; U87842; AAB94359.1; -;
DR EMBL; U87994; AAB94365.1; -;
DR EMBL; U87995; AAB94366.1; -;
DR EMBL; U88143; AAB94368.1; -;
DR HSSP; O92956; IGMA.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF000020; TNFR_C6_2.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
QO SEQUENCE 349 AA; 38295 MW; CSD2C949ED2B8E7C CRC64;

Query Match	17.1%;	Score 269.5;	DB 12;	Length 349;
Best Local Similarity	32.6%;	Pred. No. 1e-18;		

	Matches	59,	Conservative	22,	Mismatches	81,	Indels	19,	Gaps	5,
QY	21	LRLVLYLFLGAPC-----	YALALBSCKDEYFVSGSECCPKSPGIVRAEAGCEL	70						
Db	1	MSRLVLYSYILLFLSCI	IINGRDIAHPAASNGCKXNEYRSRLCCLSGCPPTGYASRLCDSK	60						
QY	71	TGYVCECPPGTYTAHLNGLSKCLQC-MCDPAMGLASRNCSTR	TENAVGCSGPGFCTIV	129						
Db	61	TNTGCTCGSGSTPFLSHNNHLQACLSGNGRCD-SNQVETRSCNTTHNR	IGCISGYYCLL	118						
QY	130	QDGDHCACPRVATSSPGQRYOKGCTESODTLCONCPPTGFS	PNGTLEBEOHQTKSMLV	189						
Db	119	KGASGGRCTSTCKTKGIGYGV-SGYTSTGDVICSPPCGPTYS-----	HTVSTDTCKEPRV	172						
QY	190	T	190							
Db	173	T	173							

RESULT 12	
057098	
ID 057098	PRELIMINARY;
	PRT; 349 AA.

DT 01-JUN-1998 (TReMBLrel_06, Created)
DT 01-JUN-1998 (TReMBLrel_06, Last sequence update)
DT 01-MAR-2003 (TReMBLrel_23, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Camel痘x virus (strain CP-1)..
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxId=203174;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Saudi-M3;
RA Loparev V.N., Parsons J.M., Eposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

```
DR HSSP: Q92956; 1MA.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00650; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 349 AA; 37978 MW; 8630EFAED7A584B5 CRC64;
```

Query Match 16.9%; Score 266.5; DB 12; Length 349;
 Best Local Similarity 33.1%; Pred. No. 2, 1e-18;
 Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

```

QY      21 LRVLVLTFLFGAFC-----YAPALPSCKEDEYPVSGECCPKSCPGYRVEACGEL 70
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1 MKSVLYSYILFLSCIIINGRDVTPYAPASNGCKDNEYKRNHLCCLSCEPGFYASRLDSDK 60

QY      71 TGIVCEPCPPGTITAHNGISKLCQQ--MDDPAMGLBASNCSTENAVCGCSFGHCTIV 129
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      61 TINTQCTPGCGGFTSRNNHLPACTLSCNGRCD--SNQVETRSCTYTHRIICECSPGYYCIL 118

QY      130 QDDPHCAACRAYATSPGQRVQKGGTESOOTLCONCPGFGSPN--GTLREQO 180
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      119 KGSSEGCACACYSQTKCGIGYGV--SGHTSAGVITCSFCLGYTSKRVTSADCKE 169
  
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RESULT 13	
057284	
ID	PRELIMINARY; PRT; 349 AA.
057284	AC
DT 01-JUN-1998	(TREMblurel. 06, Created)
DT 01-JUN-1998	(TREMblurel. 06, Last sequence update)
DT 01-MAR-2003	(TREMblurel. 23, Last annotation update)

KW	Receptor	Seq	Score	DB	Length	Matches	Similarity	Pred. No.	Mismatches	Indels	Gaps
SO	SEQUENCE	348 AA;	38212 MW;	E555979057DEC91F	CRC64;	17.1%;	32.6%;	1e-18;	78;	15;	5
Qy	Query Match	Best Local	Similarity	32.6%;	Pred. No.	1e-18;	78;	Indels	15;	Gaps	5
Db	Matches	57;	Conservative	25;	Mismatches	78;	Indels	15;	Gaps	5	
Qy	21	LRLVLYLTLGAPC-----YAPALPSCKEDEYVPGSECCPKCSFGYRKAKCGEL	70								
Db	1	MSRVLSYSLTFLSCIIINGRDIAFPAPFNSNGKCKDNEYSRNLCCLSCPGPTVARSILCSK	60								
Qy	71	TGTGCEPCPPGTYVHLNGLSKCLQCQ--MCDPAMGLARSNCSTRENAVCGSPGHFIC	129								
Db	61	TNTQCTPGSGDFTSHNNHLOACLSCNCRCD--SNQVERSCNTHNRKLCESPGYCYLL	118								
Qy	130	QGDHCAACRAAYATSSPGQRYQKGTGESODTLQCNCPFTSPFN--GILECCQHOT	183								
Db	119	KGSQSGCRCTISKTKGIGIGYV--SGYTSIGDVLCSPCGPGTYSHTVASIDYCKEPPVT	172								

RESULT 8	PRELIMINARY;	PRT;	348 AA.
057277			
ID	057277		
AC	057277;		
DT	01-JUN-1998 (TREMBLrel. 06, Created)		
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Tumor necrosis factor receptor II homolog (ZLR) (ZLR).		
GN	CRMB OR ZLR OR ZLR.		
OS	Monkeypox virus.		
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;		
OC	Orthopoxvirus.		
OX	NCBI_TaxID=10244;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	STRAIN=ZAIRE-1996 /96-17, and ZAIRE-1996 / 96-16;		
RA	Loparev V.N., Parsons J.M., Esposto J.J.;		
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	STRAIN=Zaire-96-I-16;		
RX	MEDLINE=21592287; PubMed=11734207;		
RA	Shchelkunov S.N., Totmenin A.V., Babkin I.V., Saifonov P.F.,		
RA	Ryzankina O.I., Petrov N.A., Gutorov V.V., Uvarova E.A.,		
RA	Mihnev M.V., Sisler J.R., Esposto J.J., Jahrling P.B., Mose B.,		
RA	Sandakhchiev L.S.;		
RT	"Human monkeypox and smallpox viruses: genomic comparison.";		
RL	FEBS Lett. 509:66-70(2001).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	STRAIN=Zaire-96-I-16;		
RA	Shchelkunov S.N., Totmenin A.V., Saifonov P.F., Gutorov V.V.,		
RA	Ryzankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,		
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; U88543; AAB94378.1; -		
DR	EMBL; U87841; AAB94358.1; -		
DR	EMBL; AF380138; AAL40648.1; -		
DR	EMBL; AF380138; AAL40640.1; -		
DR	HSSP; Q92956; IJMA.		
DR	InterPro; IPR001368; TNFR_C6.		
DR	Pfam; PF00020; TNFR_C6; 2.		
DR	SMART; PS00208; TNFR_2.		
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.		
DR	PROSITE; PS00650; TNFR_NGFR_2; 2.		
SO	SEQUENCE 348 AA; 38212 MW; 54019521556C2D8F CRC64;		
Query Match	17.1%;	Score 269.5;	DB 12; Length 348;
Best Local Similarity	32.6%;	Pred. No. 1e-18;	
Matches	57; Conservative	25; Mismatches	78; Indels 15; Gaps 5
21 LRLVLYTLFLGAPC-----YAPALPSCKEDYEPVGSBECCPCSGRYKVEACGGL 70			

Db 1 MSVLSYILFLSCIIINGRDIAHPAPNGKCKONKERRRLCCLSCDPGTVASRLDSK 60

Qy 71 TGVEPCPCPGRYIAHLGLSKLCQQ-MCPAMGLASRCRSTENAVAGCGSGHCIV 129

Db 61 INTQCTPCSGDITFTSHNHLLACLSGRCRD-SNOYETRESCNTHNRICEGSRGYCLL 118

Qy 130 QQDHCACRAVAITSSPGQRYVQKGTESQDPLCONCPGTFSFN-GLIECQHOT 183

Db 119 KSSGGRTIISTKTCGIGYV-SGTSYSGDVICSPGCGYVSHTVSSTDKCEPT 172

[illegible]

QY 141 YATSSPGQVQKGTESODTLQONCPGTFP- PNGTLEECOHQK- SMLVTKAGAGTSS 198
DB 122 HSLCPGAGVQKQMATVSDTICEPCVGFPSNVSSASEKQCPWTSCSKGLVEQAGATNK 181
QY 199 SHWVWFSSGLVIVVSTGGLICVKKRKRPGVAVYISVQKRDPAEAGEA----- 252
DB 182 TDVCGFQSRMRALVPIITIGILPA----- VLLVFLCIRKVTKEOTKALHPKTE 232
QY 253 --TVIEA--LOAPPDVTVAVEETI 273
DB 233 RQDPVETIDLEDFD-STAPVOETL 256

RESULT 5

Q8K2X6 PRELIMINARY: PRT; 289 AA.
ID 08K2X6
AC 08K2X6:
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 5.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straubeberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029254; AAH29254.1; -
DR InterPro; IPR001005; Myb DNA binding.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KM Receptor.
SQ SEQUENCE 289 AA; 32077 MW; DBE93B1E439F1E2A CRC64;

Query Match 17.8%; Score 280.5; DB 11; Length 289;
Best Local Similarity 27.9%; Pred. No. 6.6e-20;
Matches 69; Conservative 43; Mismatches 106; Indels 29; Gaps 8;

QY 41 SCDEDEPVGSECCPKSPGYRVKACGELTGTVCPEPCPGTYIAHNGSKLQCCMCD 100
DB 25 TCSDKQYLDHQCCDLQCPGSLTSHCTALEKTOCHPEDSGEFAQWNRIRHQHRC 84
QY 101 PAMLLASRNCSRERNVCGSPGHFCTVQGDHCACACRAVATSSPGQVQKGTESODT 160
DB 85 PNOGLRVKKEGTASDVTVCACKEGQHTSKD---CEACAQHTPCI PGVWEMAKETETDT 141
QY 161 LCQNCPPGTFSFNGTL-EECOHQTCS---MLVTKAGAGSSSHWVWFLSGSLVIV 215
DB 142 VCHCPCPGFSPNOSLPEKCTPMTSCEDKMLEVQK---GTSQNVICGLKSRMRALLVI 198
QY 216 CSTVGLITC-----VRR--RKRPGDVVIVSVORROBAEGEATVTEALQAPDVT 266
DB 199 PVWVGILITITIGVFLYIKVVKKPKDN--ELPPAARQDPQEME-----DYFGNTA 249
QY 267 VAVEETI 273
DB 250 APVOETL 256

RESULT 6
057100 PRELIMINARY: PRT; 349 AA.
ID 057100
AC 057100:
DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Nigeria-1971;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species."
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87844; AAB94361.1; -
DR HSSP; Q92956; JUMA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KM Receptor.
SQ SEQUENCE 349 AA; 38239 MW; DFC280D478F2422 CRC64;

Query Match 17.2%; Score 271.5; DB 12; Length 349;
Best Local Similarity 32.6%; Pred. No. 6.6e-19;
Matches 59; Conservative 23; Mismatches 80; Indels 19; Gaps 5;

QY 21 LRLVLYTLFLGAPC-----YAPALPSCKEDEVPGSECCPKSPGYRVKACGEL 70
DB 1 MRSVLVLYILFLSCIINGRDIAHPASNGCKDNEYRSNNLCLSCPPTVASRLCDSK 60
QY 71 TGYVCEPCPGTYIAHNGSKLQCC-MDPMGLASRNCSTERNVAVCGSPGHFCTV 129
DB 61 TNYQCTPGCGSDTFSSHNNHQAQCLSCNGRCD--SNQVETSCYTHNRIRCECSPGYVCL 118
QY 130 QDDGHCACRAVATSSPGQVQKGTESODTLQONCPGTFSPNGTLEECOHQTKCSMLV 169
DB 119 KGASGCTCKSKTKCGIGIV-SGYTSTGDVYCSPCPGTYI-----HTVSTDKCPV 172
QY 190 T 190
DB 173 T 173

RESULT 7

057108 PRELIMINARY: PRT; 348 AA.
ID 057108
AC 057108:
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Zaire-1970;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AAB94367.1; -
DR HSSP; Q92956; JUMA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.


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QY 61 YRYKACGELTGVCPCPCPGTYIAHNLGSKLQCOMCDPAMGLASRNCRSTENAVCG 120
DB 61 FHVRAQCGQTGVCPCPGTYIAHNLGSKLQCOMCDPAMGLASRNCRSTENAVCG 120
QY 121 CSPGHFCITVODGHCACRAVATSSPGORVOKGTSODTLCNCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCITVODGHCACRAVATSSPGORVOKGTSODTLCNCPGTFSPNGTLEECQ 180
QY 181 HQTKGS-WLVTKAGACTSSHWWMFLSGSLVIVIVCSTV--GLIICVRRKPRGVDVYK 237
DB 181 HGKCKCKMLVTEAGPCTSSSRWMMLLSGSLVIVIVGILILILICVRRKPRGVDVYK 240
QY 238 IYSVORROABEGEATVIALQAPPDVTVAVEETIPSTGTS 280
DB 241 IYSVORROABEGEATVTEAVQAPDITVAVEETIPSTGTS 283

RESULT 2
Q8N634 PRELIMINARY; PRT; 199 AA.
AC Q8N634;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 14
DE (heparin sulfate receptor).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Brain, and Lung;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC029848; AAH29848.1;
DR InterPro: IPR001368; TNR_C6.
DR Pfam: PF00020; TNR_C6; 1.
KW Receptor.
SQ SEQUENCE 199 AA; 21404 MW; F04A2264BC16D00A CRC64;

Query Match 62.0%; Score 978; DB 6; Length 199;
Best Local Similarity 99.5%; Pred. No. 3.9e-90;
Matches 182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 PAMGLASRNCRSTENAVCGSPGHFCITVODGHCACRAVATSSPGORVOKGTSODT 160
DB 17 PAMGLASRNCRSTENAVCGSPGHFCITVODGHCACRAVATSSPGORVOKGTSODT 76
QY 161 LCNCPGTFSPNGTLEECQHQTKGSWLVTKAGAGTSSHWWMFLSGSLVIVIVCSTVG 220
DB 77 LCNCPGTFSPNGTLEECQHQTKGSWLVTKAGAGTSSHWWMFLSGSLVIVIVCSTVG 136
QY 221 LIICVRRKPRGVDVYK IYSVORROABEGEATVIALQAPPDVTVAVEETIPSTGTS 280
DB 137 LIICVRRKPRGVDVYK IYSVORROABEGEATVIALQAPPDVTVAVEETIPSTGTS 196
QY 281 PNH 283
DB 197 PNH 199

RESULT 3
Q8VC17 PRELIMINARY; PRT; 196 AA.
AC Q8VC17;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 21.6 kDa protein (Fragment).
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC022125; AAH22125.1;
DR InterPro: IPR001368; TNR_C6.
DR Pfam: PF00020; TNR_C6; 3.
DR SMART: SM00208; TNR_C6; 3.
DR PROSITE: PS00500; TNR_NGFR_2; 1.
DR Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 196 AA; 21555 MW; 2AB3F8905E260E8 CRC64;

Query Match 24.4%; Score 384.5; DB 11; Length 196;
Best Local Similarity 42.4%; Pred. No. 1.5e-30;
Matches 84; Conservative 24; Mismatches 73; Indels 17; Gaps 4;

QY 82 TYIAHNLGSKLQCOMCDPAMGLASRNCRSTENAVCGSPGHFCITVODGHCACRAV 141
DB 2 TYIAHNLGSKLQCOMCDPAMGLASRNCRSTENAVCGSPGHFCITVODGHCACRAV 61
QY 142 ATSSPGORVOKGTSODTLCNCPGTFSPNGTLEECQHQTKGSWLVTKAGAGTSS---- 197
DB 62 TTCPPGQVKKRGTHDQIVCADCLGTFTSLGCTDECLPWNCSAFQGVVRRGNTSTPT 121
QY 198 --SSHWWMFLSGSLVIVIV--CSTVGLIICVRRKPRGVDVYK IYSVORROABEGEATV 254
DB 122 TCSQVYVYVSIILPLVIVGVGIAGFLICTRRHLSVAKLEPFOEQOE----- 174
QY 255 IEALQAPPDVTVAVEET 272
DB 175 -NTIRFP--VTEVGPAET 189

RESULT 4
Q8SQ34 PRELIMINARY; PRT; 278 AA.
AC Q8SQ34;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CD40.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCB1_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC West K.A., Li A.W., Rowden G.;
RL "Characterization of the Porcine CD40 Molecule."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF248545; AAL92924.1;
DR InterPro: IPR001368; TNR_C6.
DR Pfam: PF00020; TNR_C6; 4.
DR SMART: SM00208; TNR_C6; 4.
DR PROSITE: PS00652; TNR_NGFR_1; 1.
DR PROSITE: PS00500; TNR_NGFR_2; 4.
SQ SEQUENCE 278 AA; 30951 MW; 20D446B4AF93DD2 CRC64;

Query Match 21.0%; Score 332; DB 6; Length 278;
Best Local Similarity 31.7%; Pred. No. 4.2e-25;
Matches 84; Conservative 46; Mismatches 109; Indels 26; Gaps 8;

QY 21 LRLVLYLTFGLAPCAPALPSCKEDEYPVGSCPCPGYVKEACGELTGVCPCPP 80
DB 6 LKCLLMGCFLLTVHBEPP--TSCKENQYPTNSCCMLCPGQGLVNHCTVETELCPSS 64
QY 81 GTYIAHNLGSKLQCOMCDPAMGLASRNCRSTENAVCGSPGHFCITVODGHCACRA 140
DB 65 SEFLATWNRKCHQHKYCDPMLGLQVQREGTSKIDTTVCVSGEHHHC--TNSACSSCTL 121
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28-FEB-2003 (Rel. 41, Last annotation update)
 DE Soluble TNF receptor II precursor (cytokine response modifying protein
 B).
 GN (CRMB1 OR D2L) AND (CRMB2 OR H4R).
 OS Cowpox virus (CPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GRI-90 / Grishak.
 RX MEDLINE=98229462; PubMed=9568042;
 RA Shchelkunov S.N., Saitonov P.F., Totmenin A.V., Petrov N.A.,
 RY Ryzankina O.I., Gutovov V.V., Kotwal G.J.;
 RA "The genomic sequence analysis of the left and right species-specific
 RT terminal region of a cowpox virus strain reveals unique sequences and
 RT a cluster of intact ORFs for immunomodulatory and host range
 RT proteins.";
 RL Virology 243:432-460(1998).
 RN [2]
 RP FUNCTION.
 RC STRAIN=Brighton red;
 RX MEDLINE=94378510; PubMed=8091665;
 RA Hu F.Q., Smith C.A., Pickup D.J.;
 RT "Cowpox virus contains two copies of an early gene encoding a soluble
 RL secreted form of the type II TNF receptor.";
 RT Virology 204:343-356(1994).
 CC -1- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
 CC the modification of TNF-mediated antiviral processes.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.
 CC -----
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 CC -----
 DR EMBL: Y11842; CAA72578.1; -
 DR EMBL: Y15035; CAA75306.1; -
 DR HSSP: O14763; 1D0G.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00020; TNFR_C6; 2.
 DR SMART: SM00208; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00500; TNFR_NGFR_2; 2.
 DR Receptor; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 351 SOLUBLE TNF RECEPTOR II.
 FT REPEAT 31 67 TNFR-CYS 1.
 FT REPEAT 69 110 TNFR-CYS 2.
 FT DISULFID 32 43 BY SIMILARITY.
 FT DISULFID 44 57 BY SIMILARITY.
 FT DISULFID 47 67 BY SIMILARITY.
 FT DISULFID 70 85 BY SIMILARITY.
 FT DISULFID 88 102 BY SIMILARITY.
 FT DISULFID 92 110 BY SIMILARITY.
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 351 AA; 38253 MW; 57CAE73EF4B5D7C7 CRC64;
 Query Match 15.4%; Score 243.5; DB 1; Length 351;
 Best Local Similarity 31.0%; Pred. No. 2,1e-12;
 Matches 54; Conservative 27; Mismatches 76; Indels 17; Gaps 6;
 QY 21 LRLVLYLFLGAPC-----YAPALPSCKEDEYVSGCCPKSPGRVVEAGCEL 70
 DB 1 MKSLVSYILFLSCIINGRDIADHAPSNGCKDNEYNRHNLCLSCPPGYVASRLDSSK 60
 QY 71 --TGTVCPCPPGYIAHLNGLSKLCCQ--MCDPAMGLASRNCSTRENNAVCGSPGHFC 127

61 TTNITQCTPGSCGFSTRNHLPAFLCSNGRCD--SNQVETRSCNTTHNRICECAPGYGC 118
 QY 128 IVOGDHCACRAATATSSPGQVOKGTESODTLCNCPPTGSPN-GTLEECQ 180
 DB 119 LKSSGCKACVSSQTKCGIGGV-SGHTSTGDVVCSPCGTGYSHTVSADKCE 171
 RESULT 13
 TNFR4_RAT
 ID TNFR4_RAT STANDARD; PRT; 271 AA.
 AC P15725;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
 DE receptor) (OX40 antigen) (MRC OX40).
 GN TNFRSF4 OR TXGPIL OR OX40.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=90214614; PubMed=2157591;
 RA Mallett S., Fossum S., Barclay A.N.;
 RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
 RT lymphocytes - a molecule related to nerve growth factor receptor.";
 RL EMO J. 9:1063-1068(1990).
 CC -1- FUNCTION: Receptor for TNFRSF4/OX40L/GP14.
 CC -1- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAFs (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
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 CC -----
 DR EMBL: X17037; CAA34897.1; -
 DR PIR: S12783; S12783.
 DR HSSP: O14763; 1D4V.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00020; TNFR_C6; 3.
 DR SMART: SM00208; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00500; TNFR_NGFR_2; 2.
 DR Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 271 TUMOR NECROSIS FACTOR RECEPTOR
 FT DOMAIN 20 210 SUPERFAMILY MEMBER 4.
 FT TRANSMEM 211 235 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 25 60 TNFR-CYS 1.
 FT REPEAT 61 102 TNFR-CYS 2.
 FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).
 FT REPEAT 124 164 TNFR-CYS 4.
 FT DISULFID 26 37 BY SIMILARITY.
 FT DISULFID 38 51 BY SIMILARITY.
 FT DISULFID 41 59 BY SIMILARITY.
 FT DISULFID 62 76 BY SIMILARITY.
 FT DISULFID 79 94 BY SIMILARITY.
 FT DISULFID 82 102 BY SIMILARITY.
 FT DISULFID 104 122 BY SIMILARITY.
 FT DISULFID 125 138 BY SIMILARITY.
 FT DISULFID 144 163 BY SIMILARITY.
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143

Matches 69; Conservative 16; Mismatches 88; Indels 22; Gaps 8;

QY 16 PRDVLRLVLYLFLGAPCAPALPSCKE-DEYP-----VGSE-CCPKSPGGRVYEAAG 68
 DB 7 PGLSLCLVLYALPAL---LFPVAVRGVALEPTYPWDAETGERLVYAQCPCPGTFVGRPCR 63
 QY 69 ELTGTCVCEPCPGPTVIAHLNGLSKCLQCQCMCDPAMGLR--ASRNCSTRENAVCGSPGHF 126
 DB 64 RDSPTTCGPRPHNYQFWNYLRL---CRCNVLCGEREELAAACIATINRACRGTGFF 120
 QY 127 CIVQDDHCAACRAVATSSPGRVQKGTESQDTLCCPCPGTFPS-PNGTLEECQHQTQC 185
 DB 121 A-----HAGFCLHASCPCGAGVIAVGRPSQNTQCCPCPGTFPSASSSSSEQCQPHRC 174
 QY 186 SMVTVKAGAGTSSSH 200
 DB 175 TALGLALNVPGSSSH 189

RESULT 11
 ID TNR3_MOUSE STANDARD; PRT; 415 AA.
 AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (lymphotoxin-beta receptor).
 GN LTBR OR TNFRSF3 OR TNFCR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CVB; TISSUE=Lung;
 RX MEDLINE=96072804; PubMed=7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.U., Ware C.F.;
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 RT and expression.";
 RL J. Immunol. 155:5280-5288 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96153885; PubMed=8586432;
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Saseyama S.,
 RA Honjo T.;
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 RT sequence trap and chromosomal mapping.";
 RL Genomics 30:312-319 (1995).
 RN [3]
 RP INTERACTION WITH TRAF5.
 RC STRAIN=BALB/C;
 RX MEDLINE=96278943; PubMed=8663299;
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
 RA Yagita H., Okumura K.;
 RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
 RT the lymphotoxin-beta receptor.";
 RL J. Biol. Chem. 271:14661-14664 (1996).
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and LTb. and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF5. May play a role in the development of lymphoid organs
 CC (By similarity).
 CC -1- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.
 CC Associates with TRAF3 and TRAF4 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
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CC EMBL: U29173; AAA68964.1; -
 CC EMBL: L38423; AAB00846.1; -
 CC DR EMBL: U30798; AAA81334.1; -
 CC DR HSSP: O14763; 1D0G.
 CC DR MGD: MG1:104875; Ltbr.
 CC DR InterPro: IPR001368; TNFR_c6.
 CC DR Pfam: PF00020; TNFR_c6; 3.
 CC DR SMART: SM00208; TNFR; 3.
 CC DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 CC DR PROSITE: PS00500; TNFR_NGFR_2; 3.
 CC KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 415
 FT FT
 FT DOMAIN 31 223
 FT TRANSMEM 224 244
 FT DOMAIN 245 415
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 170
 FT REPEAT 171 213
 FT DISULFID 43 58
 FT DISULFID 59 72
 FT DISULFID 62 80
 FT DISULFID 83 98
 FT DISULFID 101 116
 FT DISULFID 104 124
 FT DISULFID 126 132
 FT DISULFID 139 150
 FT DISULFID 142 169
 FT DISULFID 172 187
 FT CARBOHYD 40 40
 FT CARBOHYD 179 179
 FT SEQUENCE 415 AA; 44956 MW; 298326A56AEF61 CRC64;

Query Match 15.6%; Score 245.5; DB 1; Length 415;
 Best Local Similarity 25.9%; Pred. No. 1,7e-12;
 Matches 83; Conservative 40; Mismatches 115; Indels 83; Gaps 15;

QY 7 WGP-----PPMSPTPTDVLRLVLYLFLGAPCAPALPSCKEDEY-- 47
 DB 14 WGPLLGLSLGLVAQPOLVPPRYENQT-----CMD-----QDKELYE 52
 QY 48 PVGSECCPKSPGGRVYKACGELGTVCPCPGPTVIAHLNGLSKCLQCQCMCDPAMGLR 107
 DB 53 PMHDVCCSRCPGGEFVFAVCSRSQDTVCKTCHNSYNEHMHLSITCOLCRPCDIVLGFEE 112
 QY 108 SRNCSTRENAVCGSPGHFCIVQDD--HCAACRAVATSSPGRVQKGTESQ----- 158
 DB 113 VAPCTSDRAKRCRCOPGMSCVYLDNECVACHEERLV-----LCQPTAEAVTDEIMD 164
 QY 159 -DTLCCNCPGTF-----SPNGTLEECQHQTCSWL-VTKAGAGTSSSHV----- 202
 DB 165 TVNVCVPCKPGHFOUNTSPRA---RCQPTREIGLVLAAGTISDITCKNPPRGAM 221
 QY 203 -WVFLSGSLVIVIVSTVGLICVKKRPRGDVVKVIVSVORKROAEAGATVIALQAP 261
 DB 222 LLLAILSLVLLFLFTV--LACAWMRHP--SLCRKLGLTLKRHPGE-ESPPCAPRAD 276
 QY 262 PDVTYVAVEETPSFGRSPN 282
 DB 277 PHEPDLA-BPLPMSGDLSPS 296

RESULT 12
 ID CRMB_COMPX STANDARD; PRT; 351 AA.
 AC 073559;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

Db 117 TSKRTQRCOPGMECAAM-ALECHCELLSDCPGTEALKEDEVGKNNH-----CVPC 170
 Oy 166 PPGTF-----SPNGTLEBEOHQTKC-SWLVTKAGACTSSHHWYV-----FLSGSLVI 212
 Db 171 KAGHQNNTSSPSA-----RCQPHRCENOGILVEAPPTAGSDPTCKKPLPLEPPENSGTLM 227
 Oy 213 VIVCTVGLIIT-----CVKRRKRGDVVKYIVORRQROAEATVITLQAP----- 261
 Db 228 LAVLLPLAFPLLATVFCSCIMWSPH--SLCRKLGLSLKRRRPGEGPNVAGSWEPPKAP 285
 Oy 262 --PDVTVAVEETIPSTFGTSP 281
 Db 286 YFPDL-----VQPLPISGDVSP 303

RESULT 10
 TR6B_HUMAN
 ID - TR6B_HUMAN STANDARD; PRT; 300 AA.
 AC 095407;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor, receptor superfamily member 6B precursor (Decoy receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M68).
 GN TNFRSF6B OR DCR3 OR TR6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal lung;
 RA MEDLINE=99087326; PubMed=9872321;
 RA Picti R.M., Marsers S.A., Lawrence D.A., Roy M., Kischkel F.C., Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T., Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L., Goddard A.D., Botstein D., Ashkenazi A.;
 RT "Genomic amplification of a decoy receptor for Fas ligand in lung and colon cancer";
 RL Nature 396:699-703 (1998).
 RL [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
 RC TISSUE=Prostate;
 RX MEDLINE=99253915; PubMed=10318773;
 RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Bner R., Kwon B.S.;
 RT "A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis";
 RL J. Biol. Chem. 274:13733-13736 (1999).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA MEDLINE=20122600; PubMed=10655513;
 RA Bal C., Connolly B., Metzker M.L., Hiliard C.A., Liu X., Sandig V., Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
 RT "Overexpression of M68/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235 (2000).
 RL [4]
 RP SEQUENCE FROM N.A.
 RA Matthews L.;
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 RL [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung, and Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L., Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC - FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT and TNFRSF6/FasL. Protects against apoptosis.
 CC - SUBCELLULAR LOCATION: Secreted.
 CC - TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
 CC Detected in adult stomach, spinal cord, lymph node, trachea, spleen, colon and lung. Highly expressed in several primary tumors from colon, stomach, rectum, esophagus and in SW480 colon carcinoma cells.
 CC - SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
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 CC -----
 DR EMBL; AF104419; AAD03056.1; -;
 DR EMBL; AF134240; AAD29688.1; -;
 DR EMBL; AF177796; AAF35244.1; -;
 DR EMBL; AF217793; AAF33685.1; -;
 DR EMBL; AF217794; AAF33686.1; -;
 DR EMBL; AL121845; CAC03668.1; -;
 DR EMBL; BC017065; AAH17065.1; -;
 DR EMBL; BC034349; AAH34349.1; -;
 DR HSP; O14763; IDOG.
 DR Genew; HGNC:11921; TNFRSF6B.
 DR MIM; 603361; -;
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0006946; P:anti-apoptosis; TAS.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1
 FT CHAIN 30 300
 FT REPEAT 31 70
 FT REPEAT 72 113
 FT REPEAT 115 150
 FT REPEAT 152 193
 FT DISULFID 49 62
 FT DISULFID 52 70
 FT DISULFID 73 88
 FT DISULFID 91 105
 FT DISULFID 95 113
 FT DISULFID 115 126
 FT DISULFID 132 150
 FT DISULFID 153 168
 FT DISULFID 174 193
 FT CARBOHYD 173 173
 SQ SEQUENCE 300 AA; 32679 MW; F90ABE337718449AF CRC64;
 N-LINKED (GLCNAC...) (POTENTIAL).
 Query Match 15.6%; Score 246; DB 1; Length 300;
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NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Liver;
 MEDLINE=9325381; PubMed=8486360;
 Baens M., Chaffener M., Cassman J.J., den Bergh H., Marynen P.;
 "Construction and evaluation of a huncDNA library of human 12p
 transcribed sequences derived from a somatic cell hybrid."
 Genomics 16:214-218(1993).
 [2]
 SEQUENCE FROM N.A.
 TISSUE=Lung;
 MEDLINE=22388257; PubMed=12477932;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 Brownstein M.J., Udén T.B., Toshyuk S., Carninci P., Prange C.,
 Rana S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McQuellan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Holton E., Kettelman M., Madsen A., Rodriguez S., Sanchez A.,
 Whiting M., Madsen A., Young A.C., Shevchenko Y., Boulford G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butlerfield Y.S.N., Krzyzanski M.I., Skalska U., Smalins D.E.,
 Schenker A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences."
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [3]
 FUNCTION.
 MEDLINE=94225209; PubMed=8171323;
 Crowe P.D., Vanhrsedale T.L., Walter B.N., Ware C.F., Hession C.,
 Ehrenfele B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
 A lymphotoxin-beta-specific receptor."
 Science 264:707-710(1994).
 [4]
 CHARACTERIZATION.
 MEDLINE=99223511; PubMed=10207006;
 Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
 "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
 death in HeLa cells."
 J. Biol. Chem. 274:11868-11873(1999).
 [5]
 FUNCTION.
 MEDLINE=20261554; PubMed=10799510;
 Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.;
 Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
 "Lymphotoxin-beta receptor is necessary and sufficient for
 LIGHT-mediated apoptosis of tumor cells."
 J. Biol. Chem. 275:14307-14315(2000).
 [6]
 INTERACTION WITH TRAF3.
 MEDLINE=96278943; PubMed=8663299;
 Nakano H., Oshima H., Chung W., Williams-Abbot L., Ware C.F.,
 Yada H., Okumura K.;
 "TRAF3, an activator of NF-kappaB and putative signal transducer for
 the lymphotoxin-beta receptor."
 J. Biol. Chem. 271:14661-14664(1996).
 [7]
 INTERACTION WITH TRAF4.
 PubMed=9626059;
 Krajewska M., Krajewski S., Zapata J.M., Vanhrsedale T.,
 Gracjewska R.D., Berern K., McFadden R., Shabak A., Hugh J.,
 Reynolds A., Cleveland C.V., Reed J.C.;
 "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
 adult, fetal, and tumor tissues."
 Am. J. Pathol. 152:1549-1561(1998).
 [8]

```

RP INTERACTION WITH TRAF5.
RX MEDLINE=98172745; PubMed=9511754;
RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA Otsuka M., Yamamoto T., Inoue U.-I.;
RT "Cloning and characterization of a cDNA encoding the human homolog of
RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL Gene 207:135-140(1998) .
CC - FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTN and LTβ, and for TNFα514/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs.
CC - SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
CC - SIMILARITY: Contains 4 TNFR-Cys repeats.
-----
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CC EMBL; L04270; AAA6757.1; -.
DR EMBL; BC026262; AAH26262.1; -.
DR PIR; I54182; I54182.
DR HSSP; P25942; 1CDF.
DR Genew; HGNC:6718; LTBR.
DR MIM; 600979; -.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPRO01368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 3.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 435
FT FT 31 435
FT DOMAIN 31 227
FT TRANSMEM 228 248
FT DOMAIN 249 435
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 168
FT REPEAT 169 211
FT DISULFID 43 58
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FT DISULFID 72 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 148
FT DISULFID 142 167
FT DISULFID 170 185
FT CAROXYD 40
FT CAROXYD 177
SQ SEQUENCE 435 AA; 46709 MW; 62462656022F656F CRC64;
Query Match 16.0%; Score 253; DB 1; Length 435;
Best Local Similarity 26.7%; Pred. No. 4,6e-13;
Matches 86; Conservative 37; Mismatches 127; Indels 72; Gaps 16
4 PG-DWGPEPMWSTPRTDVLRLVLYLTFL-----GAPCYALPFSCK--EDFY--PVGS 51
10 PGLAMP-----LVLGFLGLAAGPOAVPYASBNQCRQDEKEYEYEPQR 56
52 ECPCPKSGRYRKEACGELGTVCSPCPPTGYIAHLNGSKLCQCQCDPANGLRASRNC 111
57 ICSCRCPPTGYVSACSRSIRDVTVCATCAENSINEHNMYLLITCOLCRPCDPVNGLEIAPC 116
112 SRTEAVVGCGSGHGHCIVODGDGHCAACRAYATSSRG-----QRVKGGETSDTLICNC 155

```


DE Soluble TNF receptor II precursor (cytokine response modifying protein
 DE B).
 GN CRM8 OR G2R OR GAR.
 OS Variola virus.
 CC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 CC Orthopoxvirus.
 OK NCBI_taxid=10255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=India-1967 / Isolate Ind3;
 RX MEDLINE=9320281; PubMed=8384129;
 RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
 RT "Genes of variola and vaccinia viruses necessary to overcome the host
 RT protective mechanisms.";
 RL FEBS Lett. 319:80-83(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bangladesh-1975;
 RX MEDLINE=94088747; PubMed=8264798;
 RA Maesung R.F., Esposito J.J., Liu L., Qi J., Uteerback T.R.,
 RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
 RA Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
 RA Venter C.J.;
 RT "Potential virulence determinants in terminal regions of variola
 RT smallpox virus genome.";
 RL Nature 366:748-751(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Garcia-1966, and Somalia-1977;
 RA Maesung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
 RA Totmenin A.V., Shchelkunov S.N., Esposito J.J.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Garcia-1966;
 RX MEDLINE=20107289; PubMed=10639322;
 RA Shchelkunov S.N., Totmenin A.V., Loparev V.N., Satornov P.F.,
 RA Gutorov V.V., Chizhikov V.E., Knight J.C., Parsons J.M., Maesung R.F.,
 RA Esposito J.J.;
 RT "Alastrim smallpox variola minor virus genome DNA sequences.";
 RL Virology 266:361-386(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RT "DNA sequence analysis as a criterion for allocation of the
 RT orthopoxviruses to a particular species.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
 CC the modification of TNF-mediated antiviral processes (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.
 CC
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 CC
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 DR EMBL: X69198; CAA49137.1; -
 DR EMBL: X67117; CAA47540.1; -
 DR EMBL: L22579; AAA60933.1; -
 DR EMBL: U18339; AAA69407.1; -
 DR EMBL: U18341; AAA69467.1; -
 DR EMBL: Y16780; CAB54798.1; -
 DR EMBL: U88146; AAB94371.1; -
 DR EMBL: U88148; AAB94373.1; -
 DR EMBL: U88149; AAB94374.1; -
 DR EMBL: U88152; AAB94377.1; -
 DR PIR: D36858; D36858.

DR PIR: D72175; D72175.
 DR PIR: T28623; T28623.
 DR HSSP: O14763; 1D0G.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00650; TNFR_NGFR_2; 2.
 KW Receptor; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 349
 FT REPEAT 31 66
 FT REPEAT 67 108
 FT DISULFID 32 43
 FT DISULFID 44 57
 FT DISULFID 47 65
 FT DISULFID 68 83
 FT DISULFID 86 100
 FT DISULFID 90 108
 FT CARBOHYD 101 101
 FT CARBOHYD 173 173
 FT CARBOHYD 189 189
 FT CARBOHYD 215 215
 FT CARBOHYD 248 248
 FT CARBOHYD 17 17
 FT VARIANT 160 160
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 FT VARIANT 182 182
 FT VARIANT 274 274
 FT VARIANT 335 335
 FT VARIANT 339 339
 FT SEQUENCE 349 AA; 38189 MW; D45D40B5C6E780BF CRC64;
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 Query Match 16.3%; Score 257; DB 1; Length 349;
 Best Local Similarity 29.3%; Pred. No. 1.8e-13;
 Matches 66; Conservative 23; Mismatches 94; Indels 42; Gaps 8;
 QY 21 LRLVLYTFLGAPC-----YAPALPSCKEDKDEYVSCCPKSPGVRYKEACGEL 70
 DB 1 MSLVLYIYIFLSCIINGDAAPYTPNCKCKDTEKRNLCCLSCPPTVSRLCDSK 60
 QY 71 TGIVCEPCPGPTVIAHLNGSKLQCO-MCDPAMGLASRNSRTENAVCGSPGHFCIV 129
 DB 61 TINTQCTPCGSGTFTSRNNHLPALCISGRCN--SNQVETRSCNTHNRICEGSPGYCLL 118
 QY 130 QDDGHCACAGAYATSSRQGVQKGTESQTLQONCPRTFS-----PNCITL 177
 DB 119 KGSSGCAKCAVCSQKRCIGYGV-SGHTSVGVVICSPGFGYSHTVSSADKCEPVNPTFN 177
 QY 178 ECQ-----HOTKSWLTKAGAGTSSSHWMMFISGLSVVI 214
 DB 178 YIDVETLYVNDTSCRTT---TGLSES-----ITSLTITM 214
 RESULT 9
 TNFR3_HUMAN
 ID TNFR3_HUMAN STANDARD; PRT; 435 AA.
 AC P36941;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
 DE protein) (Tumor necrosis factor C receptor).
 GN LTRR OR TNFRSF3 OR TNFCR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors." ;
RL J. Biol. Chem. 265:1531-1536 (1990).
RN [8]
RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RX MEDLINE=91056048; PubMed=2173696;
RA Boeckner H., Schlaeger E.J., Lamm H.-W., Pan Y.-C.E., Lesslauer W.,
R Brockhaus M.;
RT "Purification and partial amino acid sequence analysis of two
RT distinct tumor necrosis factor receptors from HL60 cells." ;
RL J. Biol. Chem. 265:20131-20138 (1990).
RN [9]
RP CHARACTERIZATION
RX MEDLINE=93015040; PubMed=1328224;
RA Pennica D., Lam V.T., Mize N.R., Weber R.F., Lewis M., Fendly B.M.,
RA Lipari M.T., Goeddel D.V.;
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT Characterization of ligand binding, internalization, and receptor
RT phosphorylation." ;
RL J. Biol. Chem. 267:21172-21178 (1992).
RN [10]
RP INTERACTION WITH TRAF2.
RX MEDLINE=94349371; PubMed=8069916;
RA Roche M., Wong S.C., Henzel W.J.;
RT "A novel family of putative signal transducers associated with the
RL cytoplasmic domain of the 75 kDa tumor necrosis factor receptor." ;
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
RD TRAF2
RX MEDLINE=99221490; PubMed=10206649;
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT "Structural basis for self-association and receptor recognition of
RL human TRAF2." ;
RN Nature 398:533-538 (1999).
RL
CC -I- FUNCTION: Receptor with high affinity for TNFRSF2/TNF-alpha and
CC approximately 5-fold lower affinity for homotrimeric
CC TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits -the
CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2.
CC
CC -I- SUBUNIT: Binds to TRAF2.
CC
CC -I- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC
CC -I- PTM: Phosphorylated; mainly on serine residues and with a very low
CC level on threonine residues.
CC
CC -I- PTM: A soluble form (tumor necrosis factor binding protein 2) is
CC produced from the membrane form by proteolytic processing.
CC
CC -I- PHARMACEUTICAL: Available under the name Enbrel (Immunex and
CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid
CC arthritis (RA). Enbrel consist of the extracellular ligand-binding
CC portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to
CC TNF-alpha and blocks its interactions with receptors.
CC
CC -I- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm";
CC -I- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
CC WWW="http://www.enbrel.com/".
CC
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CC
DR EMBL; M32315; AAAS9929.1; -;
DR EMBL; U52165; AAC50622.1; -;
DR EMBL; U52165; AAC50622.1; JOINED.
DR EMBL; U52157; AAC50622.1; JOINED.
DR EMBL; U52157; AAC50622.1; JOINED.
DR EMBL; U52158; AAC50622.1; JOINED.
DR EMBL; U52159; AAC50622.1; JOINED.
DR EMBL; U52160; AAC50622.1; JOINED.
DR EMBL; U52161; AAC50622.1; JOINED.
DR EMBL; U52162; AAC50622.1; JOINED.

ID	CRM	VAR	STANDARD	PRT	349 AA
AC	P34015	O85407	O89098	O89118	
DT	01-FEB-1994	(Rel. 28, Created)			
DT	01-FEB-1994	(Rel. 28, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DR	EMBL	U52163	AAC50622.1	JOINED	
DR	EMBL	U52164	AAC50622.1	JOINED	
DR	EMBL	M55594	AAA36755.1	-	
DR	EMBL	S63368	AAAB19624.2	-	
DR	EMBL	M53557	AAA63262.1	-	
DR	EMBL	AB030950	BAA89053.1	-	
DR	PIR	A35356	A35356	-	
DR	PDB	1CA9	12-APR-99		
DR	GeneW	HGNC:11917	TNFRSF1B		
DR	GO	GO:0005031	F: tumor necrosis factor receptor activity; TAS.		
DR	InterPro	IPR001368	TNFR_C6		
DR	Pfam	PF00020	TNFR_C6_4		
DR	SMART	SM00208	TNFR_4		
DR	PROSITE	PS00652	TNFR_NGR_1; 2.		
DR	PROSITE	PS50050	TNFR_NGR_2; 3.		
KW	Receptor	Apoptosis	Transmembrane	Glycoprotein	Repeat
KW	Phosphorylation	Pharmaceutical	Polymorphism	3D-structure	
FT	SIGNAL	1	22		
FT	CHAIN	23	461		
FT	FT				
FT	CHAIN	27	?		
FT	DOMAIN	23	257		
FT	TRANSMEM	258	287		
FT	DOMAIN	288	461		
FT	REPEAT	39	76		
FT	REPEAT	77	118		
FT	REPEAT	119	162		
FT	REPEAT	163	201		
FT	DISULFID	40	53		
FT	DISULFID	54	67		
FT	DISULFID	57	75		
FT	DISULFID	78	93		
FT	DISULFID	96	110		
FT	DISULFID	100	118		
FT	DISULFID	120	126		
FT	DISULFID	134	143		
FT	DISULFID	137	161		
FT	DISULFID	164	179		
FT	CARBOHYD	171	171		
FT	CARBOHYD	193	193		
FT	VARIANT	196	196		
FT	VARIANT	232	232		
FT	CONFLICT	141	141		
FT	CONFLICT	363	363		
FT	SEQUENCE	461 AA	48291 MW	603D0AE1CD69ACBF	CRC64
Query Match		16.4%	Score 259	DB 1	Length 461
Beat Local Similarity		32.8%	Pred. No. 1.6e-13		
Matches	59	Conservative	23	Mismatches	76
				Indels	22
				Gaps	6
QY	35	YAPALPS-CKEDEY--PVGSECCPRKCSGYRYKACGGLTGTVCPEPCPGTYIAHLNGLS	91		
DB	32	YAPFEGSTCRREYYDDQTAQWCKSCSKSGOHAKEYFCTTSPSTVDCSCBDSYTTOLMNWVP	91		
QY	92	KCLQCGMDDPAMGRASRN-----CSTENAVAGCSPGHFCYVDGPHCAACRAYATSS	145		
DB	92	ECLSS-----GSHCSSDYQVETQACTREONRITCTCRGWYCALSKQEGCRCLAPLRKR	144		
QY	146	PGORVOKGTESSODTLCONCPPTGTF--PNGTLEECOHOTKCSMLVTXKAG-----TSSS	199		
DB	145	PGFGVARGTETSDVCKPCAPAGTFNSNTTSSIDICRPHQICNVVAIPGNASMDAVCTSTS	204		
RESULT 8					
CRM	VAR				
AC	P34015	O85407	O89098	O89118	
DT	01-FEB-1994	(Rel. 28, Created)			
DT	01-FEB-1994	(Rel. 28, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			


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RX MEDLINE=87321103; PubMed=2820128;
RA Upton C., Delange A.M., McFadden G.;
RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RL telomeric region of the Shope fibroma virus genome.";
RN Virology 160:20-30(1987).
[2]
RP FUNCTION.
RX MEDLINE=91207415; PubMed=1850261;
RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RA McFadden G., Goodwin R.G.;
RT "2 open reading frame from the Shope fibroma virus encodes a soluble
RL form of the TNF receptor.";
RN Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
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CC -----
DR EMBL; M17433; -; NOT ANNOTATED_CDS.
DR EMBL; A23727; CA001687.1; -.
DR PTR; B43692; B43692.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 2.
DR SMART; SMO0208; TNFR_3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KM Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT REPEAT 27 62 TNFR-CYS 1.
FT REPEAT 63 104 TNFR-CYS 2.
FT REPEAT 105 147 TNFR-CYS 3.
FT REPEAT 148 186 TNFR-CYS 4.
FT DISULFID 28 39 BY SIMILARITY.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 43 61 BY SIMILARITY.
FT DISULFID 64 79 BY SIMILARITY.
FT DISULFID 82 96 BY SIMILARITY.
FT DISULFID 86 104 BY SIMILARITY.
FT DISULFID 106 120 BY SIMILARITY.
FT DISULFID 123 146 BY SIMILARITY.
FT DISULFID 129 149 BY SIMILARITY.
FT DISULFID 164 185 BY SIMILARITY.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;
Query Match 16.5%; Score 260; DB 1; Length 325;
Best Local Similarity 31.5%; Pred. No. 9.5e-14;
Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

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QY 180 ---QHQTCKSWLYTKAG 193
Db 177 LYPNERSCT---TTAG 190
RESULT 7
TRIB_HUMAN STANDARD; PRT; 461 AA.
ID P20333; Q16042; Q9UHN1;
AC 01-FEB-1991 (Rel. 17, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Ectarecept)
DE [Contains: "Tumor necrosis factor binding protein 2 (TRBP11)].
CN TNFRSF1B OR TNFR2 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90260635; PubMed=2160731;
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of
RL cellular and vital proteins.";
RN Science 248:1019-1023(1990).
[2]
RP SEQUENCE FROM N.A., AND VARIANT ARG-196.
RX MEDLINE=91045991; PubMed=2172983;
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
RL naturally occurring tumor necrosis factor inhibitor.";
RN Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299745; PubMed=8661109;
RA Beltzinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA Brodeur G.M.;
RT "Physical mapping and genomic structure of the human TNFR2 gene.";
RN Genomics 35:94-100(1996).
[4]
RP SEQUENCE OF 37-461 FROM N.A.
RX MEDLINE=91370690; PubMed=1966549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
RA Brockhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RL intracellular, domain sequences.";
RN Cytokine 2:231-237(1990).
[5]
RP SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.
RX MEDLINE=90349572; PubMed=2166946;
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.W.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RL and demonstration of a shed form of the receptor.";
RN Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
[6]
RP SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
RX MEDLINE=21069356; PubMed=11197692;
RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
RT "New single nucleotide polymorphisms in the coding region of human
RL TNFR2: association with systemic lupus erythematosus.";
RN Genes Immun. 1:501-503(2000).
[7]
RP SEQUENCE OF 27-31.
RX MEDLINE=90110215; PubMed=2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human

```


RT the ligand binding domain of the human B cell receptor CD40.";
 RL Proteins 27:59-70(1997).
 RN (11)
 RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
 RX MEDLINE=98266353; PubMed=9605317;
 RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
 RA Zheng Z., Natsimhen J.H., Thomas D.;
 RT "The role of polar interactions in the molecular recognition of CD40L
 RT with its receptor CD40.";
 RL Protein Sci. 7:1124-1135(1998).
 RN (12)
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH
 RP TRAF3.
 RX PubMed=10984535;
 RA Ni C.Z., Welsh K., Leo E., Chlou C.K., Wu H., Reed J.C., Ely K.R.;
 RT "Molecular basis for CD40 signaling mediated by TRAF3.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).
 RN (13)
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH
 RP TRAF3.
 RX PubMed=12005438;
 RA Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,
 RA Satterthwaite A.C., Cheng G., Ely K.R.;
 RT "Downstream regulator TRAF3 binds to the CD40 recognition site on
 RT TRAF3.";
 RL Structure 10:403-411(2002).
 RN (14)
 RP VARIANT HIGM3 ARG-83.
 RX MEDLINE=21532985; PubMed=11675497;
 RA Ferrati S., Gillani S., Inalaco A., Al-Ghonaime A., Soresina A.R.,
 RA Loubser M., Avanzini M.A., Marconi M., Badolati R., Ugazio A.G.,
 RA Levy Y., Catalan N., Durandy A., Tbakhi A., Notarangelo L.D.,
 RA Plebani A.;
 RT "Mutations of CD40 gene cause an autosomal recessive form of
 RT immunodeficiency with hyper IgM.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).
 CC -1- FUNCTION: Receptor for TNFSFs/CD40L.
 CC -1- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 AND TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform I);
 CC secreted (isoform II).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=I;
 CC IsoId=P25942-1; Sequence=Displayed;
 CC Name=II;
 CC IsoId=P25942-2; Sequence=VSP_006472, VSP_006473;
 CC -1- TISSUE SPECIFICITY: B-cells and in primary carcinomas.
 CC -1- DISEASE: Defects in TNFRSF5 are the cause of type 3 hyper-IgM
 CC immunodeficiency (HIGM3), an autosomal recessive disorder which
 CC includes an inability of B cells to undergo isotype switching, one
 CC of the final differentiation steps in the humoral immune system,
 CC an inability to mount an antibody-specific immune response, and a
 CC lack of germinal center formation.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
 CC
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 CC
 DR EMBL; X60592; CA43045.1; -;
 DR EMBL; AL035662; CAC17670.1; -;
 DR EMBL; AJ300189; CAC29424.1; -;
 DR EMBL; BC012419; AAH12419.1; -;
 DR PIR; S04460; A60771.
 DR PDB; 1CDF; 01-APR-97.
 DR PDB; 1FLI; 14-AUG-00.

DR PDB; 1LOA; 08-FEB-00.
 DR PDB; 1CZ2; 26-SEP-01.
 DR PDB; 1D00; 31-OCT-01.
 Query Match 17.0%; Score 267.5; DB 1; Length 277;
 Best Local Similarity 26.1%; Pred. No. 2e-14;
 Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;
 QY 20 VLRLVLYLTFLGAPCVAPAL-----PSCKDEYVPVSGCCPKSPGYRVKACGELGTV 74
 Db 1 MRLPLDQVLWG--CLITAHNRPBPTRCKRKYHLINSQCCSLDQPGKLVSDCTEFLPTE 58
 QY 75 CEPSPGTYIAHLNGLSKLCQCDPAMGLASRNCRTENAVCGSPGHFCTVODGDH 134
 Db 59 CLPGESEFLDWNRETHCHQHKYCDENLGLRVQOKGTSBTDITCTCEGMHC--TSEA 115
 QY 135 CAACRAATSTPGQRVQKGTESODTLQCNCPGRTS--PGITLBECHQTKCSW--LVTK 191
 Db 116 CESCVLHRSFSGFGVQIATGVSDTICEPCPVGFSSNVASAREKCHPMTSCETKDLVYQ 175
 QY 192 AGAGTSSHWMMWFLSGSLVIVGCVGLICVKRKRPGDVVKVYSVQRKQEAEGE 251
 Db 176 Q-AGTKTDVVCQPDRLRALVVIPIIFGLFA-----ILVLVPIKKVAKKPTNK 225
 QY 252 ATVIEALQAPPDV-----TTVAVEBTI 273
 Db 226 AP--HPKQEPQELNFPDDLPGSNTAPVQETL 255
 RESULT 4
 TNRS_BOVIN STANDARD; PRT; 269 AA.
 ID AC 028203;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 5 precursor
 DE (CD40L receptor) (B-cell surface antigen CD40) (Fragment).
 GN TNFRSF5 OR CD40.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97281252; PubMed=9135560;
 RA Hixano A., Brown W.C., Estes D.M.;
 RT "Cloning, expression and biological function of the bovine CD40
 RT homologue: role in B-lymphocyte growth and differentiation in
 RT cattle.";
 RL Immunology 90:294-300(1997).
 CC -1- FUNCTION: Receptor for TNFSFs/CD40L.
 CC -1- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 AND TRAF6 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC
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 CC
 DR EMBL; U57745; AAC48710.1; -;
 DR HSSP; P25942; 1CDF.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00208; TNFR_4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 1.

DB 25 TCSDKQYLDHGGCCDDCQPSRLTSHCTALEKQCHPCDSEGSASQWNRIRCHQRHCE 84
QY 101 PAMGLASRNCSTRTENAVCGSPGHFCIVODGHCACRAVATSSPGQVQKGTSSQDT 160
DB 85 PNOGLAVKKEGTASPDVCTCKREGQCHTSKD---CEACQHTPCICPGFVMEKATETDT 141
QY 161 LCONCPRTGTPNGTL-EECQHOTKS---WLVTAGAGTSSSHVWVFLSGSLVIV 215
DB 142 VCHPCVGFSPSNOSLFEKCYPTWSCEDKNLEVLQK---GTSQTNVICGLKSMRALVY 198
QY 216 CSTVGLIC-----VKR--RKPRGDVAVIVSVQKRGAEAGCATVIEALQAPPDVT 266
DB 199 PVMGLITITFGVLYIKVKKVKKDKDN--EMLPARRQDPQME-----DYGHNTA 249
QY 267 VAVEETI 273
DB 250 APVQETL 256
RESULT 3
ID TNR5 HUMAN STANDARD; PRT; 277 AA.
AC P25942; Q9BYU0;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (CDw40) (Bp50).
GN TNFRSF5 OR CD40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=89356608; PubMed=2475341;
RA Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas.";
RL EMBO J. 8:1403-1410(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deacon R., Dhani P.D., Dunn M., Ellington A.G., Franklins C., Griffiths A., Fraser A., French L., Garner P., Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Levesaith M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Pratchalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Syamam N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tyanam A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A., Wilmington L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM II).
RX MEDLINE=21117110; PubMed=1172023;
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
RT "Regulation of Cd40 function by its isoforms generated through alternative splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM I).
RC TISSUE=ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.D., Uscid T.B., Toshlyuk S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CBP1, a relative of TRAF, in CD40 signaling.";
RL Science 267:1494-1498(1995).
RN [6]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95129692; PubMed=7530216;
RA Sato T., Irie S., Reed J.C.;
RT "A novel member of the TRAF family of putative signal transducing proteins binds to the cytosolic domain of CD40.";
RL FEBS Lett. 358:113-118(1995).
RN [7]
RP INTERACTION WITH TRAF1, TRAF2, TRAF3 AND TRAF5.
RX PubMed=9718306;
RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J., Kehry M.R.;
RT "CD40-tumor necrosis factor receptor-associated factor (TRAF) interactions: regulation of CD40 signaling through multiple TRAF binding sites and TRAF hetero-oligomerization.";
RL Biochemistry 37:11836-11845(1998).
RN [8]
RP INTERACTION WITH TRAF5.
RX MEDLINE=98172745; PubMed=9511754;
RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M., Otsuka M., Yamamoto T., Inoue U.-I.;
RT "Cloning and characterization of a cDNA encoding the human homolog of tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL Gene 207:135-140(1998).
RN [9]
RP INTERACTION WITH TRAF6.
RX PubMed=9432981;
RA Kashinawa M., Shitakata Y., Inoue J.-I., Nakano H., Okazaki K., Okumura K., Yamamoto T., Nagaoka H., Takemori T.;
RT "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates extracellular signal-regulated kinase (ERK) activity in CD40 signaling along a ras-independent pathway.";
RL J. Exp. Med. 187:237-244(1998).
RN [10]
RP 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RA Bajorath J., Aruffo A.;
RT "Construction and analysis of a detailed three-dimensional model of

ID	NAME	SEQUENCE	PT	AA
NR5_MOUSE	STANDARD		289	AA
P27512	Q99NE0; Q99NE1; Q99NE2; Q99NE3;			
01-AUG-1992	(Rel. 23, Created)			
01-OCT-1996	(Rel. 34, Last sequence update)			
15-SEP-2003	(Rel. 42, Last annotation update)			
Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (Bp50) (CDw40).				
NR5_MOUSE	CD40			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI	TaxID=10090;			
[1]				
SEQUENCE FROM N.A. (ISOFORM I).				
MDLINE=92105763; PubMed=1370315;				
Torres R.M., Clark E.A.;				
"Differential increase of an alternatively polyadenylated mRNA				
species of murine CD40 upon B lymphocyte activation."				
J. Immunol. 148:620-626 (1992).				
[2]				
REVIEWS.				
STRAIN=BALB/c;				
Torres R.M.;				
Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.				
[3]				
SEQUENCE FROM N.A. (ISOFORM I).				
STRAIN=BALB/c; TISSUE=Liver;				
MDLINE=93094586; PubMed=1261194;				
Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,				
Howard M., Cockayne D.A.;				
"Genomic structure and chromosomal mapping of the murine CD40 gene."				
J. Immunol. 149:3921-3926 (1992).				
[4]				
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS II; III; IV AND				
V).				
MDLINE=21117110; PubMed=11172023;				
Tone M., Tone Y., Fairchild P.U., Wykes M., Waldmann H.;				
"Regulation of CD40 function by its isoforms generated through				
alternative splicing."				
Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756 (2001).				
[5]				
INTERACTION WITH TRAF5.				
MDLINE=95184010; PubMed=7533327;				
Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;				
"Involvement of CRAF1, a relative of TRAF, in CD40 signaling."				
Science 267:1494-1498 (1995).				
[6]				
INTERACTION WITH TRAF5.				
MDLINE=96382484; PubMed=8790348;				
Ishida T., Tojo T., Noki T., Kobayashi N., Ohishi T., Matanabe T.,				
Yamamoto T., Inoue J.-I.;				
"TRAF5, a novel tumor necrosis factor receptor-associated factor				
family protein, mediates CD40 signaling."				
Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442 (1996).				
-1- SUBUNIT: Interacts with TRAF5 and TRAF6. Interacts with TRAF1,				
TRAF2 and TRAF6 (By similarity).				
-1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV				
and V); Secreted (isoform II).				
-1- ALTERNATIVE PRODUCTS:				
Event=Alternative splicing; Named isoforms=5;				
Name=I;				
Isoid=P27512-1; Sequence=Displayed;				
Name=II;				
Isoid=P27512-2; Sequence=VSP_006474, VSP_006475;				
Name=III;				
Isoid=P27512-3; Sequence=VSP_006477, VSP_006478;				
Name=IV;				
Isoid=P27512-4; Sequence=VSP_006479, VSP_006480;				
Name=V;				
Isoid=P27512-5; Sequence=VSP_006476;				

CC	-1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC	-----
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CC	-----
DR	EMBL; M83312; AAB08705.1; -;
DR	EMBL; M94126; AAA37404.1; -;
DR	EMBL; M94129; AAA37404.1; JOINED.
DR	EMBL; M94128; AAA37404.1; JOINED.
DR	EMBL; M94127; AAA37404.1; JOINED.
DR	EMBL; AJ401387; CAC29427.1; -;
DR	EMBL; AJ401388; CAC29428.1; -;
DR	EMBL; AJ401389; CAC29429.1; -;
DR	EMBL; AJ401390; CAC29430.1; -;
DR	PIR; A46476; A46476.
DR	HSSP; P25942; ICDF.
DR	MGI; M83366; Tnf:rsf5.
DR	Interpro; IPR001368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 4.
DR	SMART; SM00208; TNFR_4.
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.
DR	PROSITE; PS50050; TNFR_NGFR_2; 4.
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW	Alternative splicing.
FT	SIGNAL 1 19 POTENTIAL.
FT	CHAIN 20 289 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 5.
FT	DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 194 215 POTENTIAL.
FT	DOMAIN 216 289 CYTOPLASMIC (POTENTIAL).
FT	REPEAT 25 60 TNFR_CYS 1.
FT	REPEAT 61 103 TNFR_CYS 2.
FT	REPEAT 104 144 TNFR_CYS 3.
FT	REPEAT 145 187 TNFR_CYS 4.
FT	DISULFID 26 37 BY SIMILARITY.
FT	DISULFID 38 51 BY SIMILARITY.
FT	DISULFID 41 59 BY SIMILARITY.
FT	DISULFID 62 77 BY SIMILARITY.
FT	DISULFID 83 103 BY SIMILARITY.
FT	DISULFID 105 119 BY SIMILARITY.
FT	DISULFID 111 116 BY SIMILARITY.
FT	DISULFID 125 143 BY SIMILARITY.
FT	CARBOHYD 153 153 N-LINKED (GLCNAC...) (POTENTIAL).
FT	VARSPLIC 166 203 SCEDNLEVLQKGSQTNVLCGLSKRRALLVPPWG -> RPKVPDASPDASHCRDGHPHHFGVALYOKGOETKG (in isoform II).
FT	VARSPPLIC 204 289 Missing (In isoform II).
FT	VARSPPLIC 187 216 /FTid=VSP_006474.
FT	VARSPPLIC 216 234 /FTid=VSP_006476.
FT	VARSPPLIC 235 289 KVVVKRPDNDMLPPARR -> SECSGEREGGFVPEDA S (in isoform III).
FT	VARSPPLIC 216 222 /FTid=VSP_006477.
FT	VARSPPLIC 223 289 Missing (In isoform III).
FT	VARSPPLIC 223 289 KVVVKRP -> SCOETKG (in isoform IV).
FT	VARSPPLIC 223 289 /FTid=VSP_006479.
FT	VARSPPLIC 223 289 Missing (In isoform IV).
FT	VARSPPLIC 223 289 /FTid=VSP_006480.
FT	SEQUENCE 289 AA; 32111 MM; C791CB6D2FEA574E CRC64;
FT	Query Match 17.5%; Score 276.5; DB 1; Length 289;
FT	Best Local Similarity 27.9%; Pred. No. 4.1e-15;
FT	Matches 69; Conservative 43; Mismatches 106; Indels 29; Gaps 8
FT	41 SCKEDEYVPSGCCPCSGPYRVAVAGAGELGTVCCECPGPETYIAHLINGLSKLCLQCIMCD 100

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guntarine P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 RL [6]
 RN INTERACTION WITH TRAF2 AND TRAF5.
 RP PubMed=9153189;
 RX Heu H., Solovjev I., Colombero A., Elliott R., Kelley M., Boyle W.J.,
 RA "ATRA, a novel tumor necrosis factor receptor family member, signals
 RT through TRAF2 and TRAF5.";
 RT J. Biol. Chem. 272:13471-13474(1997).
 RL [7]
 RN INTERACTION WITH TRAF3 AND TRAF5.
 RP PubMed=9162022;
 RX Masters S.A., Ayres T.M., Skubatch M., Gray C.L., Rothe M.,
 RA Ashkenazi A., Ayres T.M., Skubatch M., Gray C.L., Rothe M.,
 RT "Herpesvirus entry mediator, a member of the tumor necrosis factor
 RT receptor (TNFR) family, interacts with members of the TNFR-associated
 RT factor family and activates the transcription factors NF-kappaB and
 RT AP-1.";
 RT J. Biol. Chem. 272:14029-14032(1997).
 RN [8]
 RX X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
 RL MEDLINE=21403268; PubMed=11511370;
 RA Carli A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,
 RA Eisenberg R.J., Wiley D.C.;
 RT "Herpes simplex virus glycoprotein D bound to the human receptor
 RT HxvD.";
 RL Mol. Cell 8:169-179(2001).
 CC -1- FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric
 CC TNFSF14/lymphotoxin-alpha. Involved in lymphocyte activation. Plays
 CC an important role in HSV pathogenesis because it enhanced the
 CC entry of several wildtype HSV strains of both serotypes into CHO
 CC cells, and mediated HSV entry into activated human T cells.
 CC -1- SUBUNIT: INTERACTS WITH TRAF2, TRAF3 AND TRAF5.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (probable).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
 CC IN LUNG, SPLEEN, AND THYMUS.
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; U70321; AAB58354.1; -;
 DR EMBL; U81232; AAD00505.1; -;
 DR EMBL; AF153978; AAF75588.1; -;
 DR EMBL; AF373877; AAL47717.1; -;
 DR EMBL; AF373878; AAL47718.1; -;
 DR EMBL; BC002794; AAH02794.1; -;
 DR PDB; 1JMA; 26-SEP-01.
 DR Genew; HGNC:11912; TNFRSF14.
 DR MIM; 602746; -;
 DR GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR Interpro; IPR001368; TNFR_c6; 3.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS00652; TNFR_NGFR_2; 2.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
 KM 3D-structure.
 FT SIGNAL 1 38
 FT CHAIN 39 283
 FT DOMAIN 39 202
 FT TRANSMEM 203 223
 FT DOMAIN 224 283
 FT REPEAT 42 75
 FT REPEAT 78 119
 FT REPEAT 121 162
 FT DISULFID 42 53
 FT DISULFID 54 67
 FT DISULFID 57 75
 FT DISULFID 78 93
 FT DISULFID 96 111
 FT DISULFID 99 119
 FT DISULFID 121 138
 FT DISULFID 127 135
 FT CARBOHYD 110 110
 FT CARBOHYD 173 173
 FT VARIANT 17 17
 FT VARIANT 241 241
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 FT STRAND 82 83
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 FT STRAND 94 95
 FT TURN 101 104
 FT STRAND 105 109
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 FT TURN 123 124
 FT STRAND 125 129
 FT STRAND 137 140
 FT SEQUENCE 283 AA; 30392 MW; 46CE13C2C70242C1 CRC64;
 SQ
 Query Match 99.8%; Score 1575; DB 1; Length 283;
 Best Local Similarity 99.6%; Pred. No. 1.7e-118;
 Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MBPPGDWGPMPKRSPTPTDVLRLVLYLFLGAPCAAPALPSCKEDEYPVGSCCPKCSFG 60
 DB 1 MBPPGDWGPMPKRSPTPTDVLRLVLYLFLGAPCAAPALPSCKEDEYPVGSCCPKCSFG 60
 QY 61 YRYKACGELTGTGVEPCPPGTIYIAHLNGLSKLCIQCMQDPMAGLPASRNCSTRTENAVCG 120
 DB 61 YRYKACGELTGTGVEPCPPGTIYIAHLNGLSKLCIQCMQDPMAGLPASRNCSTRTENAVCG 120
 QY 121 CSPGHFCIVQDDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSFNGTLEECQ 180
 DB 121 CSPGHFCIVQDDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSFNGTLEECQ 180
 QY 181 HQTKGWLVTXAGAGTSSHWVWMLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
 DB 181 HQTKGWLVTXAGAGTSSHWVWMLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
 QY 241 VQRKQGEAGEATVTEALQAPDVTVAVEETIPSTGSPNH 283
 DB 241 VQRKQGEAGEATVTEALQAPDVTVAVEETIPSTGSPNH 283

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 17:27:40 ; Search time 17 Seconds

(without alignments)
782.856 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 1578

Sequence: 1 MEPPDWMGPPWRSPTPTDV.....VTVAVEETIPSTGSPNH 283

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1575	99.8	283	TR14_HUMAN	Q92956 homo sapien
2	276.5	17.5	289	TRN5_MOUSE	P27512 mus musculu
3	267.5	17.0	277	TRN5_HUMAN	P25942 homo sapien
4	267	16.9	269	TRN5_BOVIN	Q28203 bos taurus
5	266.5	16.9	349	CRMB_CAMPS	Q8UYA7 camelopox vi
6	260	16.5	325	VT2_SFVYA	P25943 Shope fibro
7	259	16.4	461	TR1B_HUMAN	P20333 homo sapien
8	257	16.3	349	CRMB_VARY	P34015 variola vir
9	253	16.0	435	TRN3_HUMAN	P36941 homo sapien
10	246	15.6	300	TR6B_HUMAN	O5407 homo sapien
11	245.5	15.6	415	TRN3_MOUSE	P50284 mus musculu
12	243.5	15.4	351	CRMB_COMPX	O73559 compox viru
13	240.5	15.2	271	TRN4_RAT	P15725 rattus norv
14	238.5	15.1	326	VT2_MXVVL	P25825 myxoma viru
15	236	15.0	332	TRN6_PIG	O77736 sus scrofa
16	215.5	13.7	272	TRN6_MOUSE	P47741 mus musculu
17	213.5	13.5	417	TR1B_MOUSE	Q940W1 mus musculu
18	213.5	13.5	474	TR1B_MOUSE	P25119 mus musculu
19	210	13.3	401	TR1B_HUMAN	O00300 homo sapien
20	209.5	13.3	616	TR11_HUMAN	Q9Y696 homo sapien
21	206.5	13.1	324	TRN6_RAT	Q61199 rattus norv
22	206.5	13.1	417	TR25_HUMAN	Q93038 h tumor nec
23	206	13.1	335	TRN6_HUMAN	P25445 homo sapien
24	205	13.0	327	TRN6_MOUSE	P25446 mus musculu
25	205	13.0	655	TR21_HUMAN	O75509 homo sapien
26	204	12.9	401	TR1B_MOUSE	O08712 mus musculu
27	203.5	12.9	425	TR16_RAT	O08727 rattus norv
28	201	12.7	401	TR1B_RAT	O08727 rattus norv
29	200.5	12.7	323	TRN6_BOVIN	P18516 bos taurus
30	198.5	12.6	416	TR16_CHICK	P18519 gallus galli
31	198.5	12.6	625	TR11_MOUSE	O35305 mus musculu
32	196	12.4	655	TR21_MOUSE	Q96PUS mus musculu
33	194.5	12.3	277	TRN4_HUMAN	P43489 homo sapien

34	192	12.2	461	TR1A_RAT	P22934 rattus norv
35	190	12.0	427	TR16_HUMAN	P08138 homo sapien
36	176.5	11.2	256	TRN9_MOUSE	P20334 mus musculu
37	173	11.0	498	TRN8_MOUSE	O60846 mus musculu
38	172.5	10.9	461	TR1A_PIG	P50555 sus scrofa
39	171.5	10.9	471	TR1A_BOVIN	O19131 bos taurus
40	171	10.8	250	TRN7_MOUSE	P41272 mus musculu
41	168.5	10.7	454	TR1A_MOUSE	P25118 mus musculu
42	168	10.6	176	TR23_MOUSE	O96162 mus musculu
43	161	10.2	180	TR22_MOUSE	O96162 mus musculu
44	161	10.2	255	TRN9_HUMAN	O07011 homo sapien
45	159	10.1	595	TRN8_HUMAN	P28908 homo sapien

ALIGNMENTS

RESULT 1

ID	TR14_HUMAN	STANDARD;	PRT;	283 AA.
AC	Q92956; Q8WXR1; Q96J31; Q9UM65;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 14 precursor			
DE	(Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)			
DE	(TR2).			
GN	TRNRSF14 OR HVEM OR HVFA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cervical adenocarcinoma;			
RX	MEDLINE=97053782; PubMed=898196;			
RA	Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;			
RT	"Herpes simplex virus-1 entry into cells mediated by a novel member of			
RT	the TNF/NGF receptor family.";			
RL	Cell 87:427-436(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97306336; PubMed=9162061;			
RA	Wang S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-U.,			
RA	Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,			
RT	Porter T.G., Truneh A., Young P.R.,			
RT	"A newly identified member of the tumor necrosis factor receptor			
RT	superfamily with a wide tissue distribution and involvement in			
RT	lymphocyte activation.";			
RL	J. Biol. Chem. 272:14272-14276(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Zhang W., Wan T., Cao X.,			
RL	Submitted (May-1999) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.			
RX	MEDLINE=21629477; PubMed=11756979;			
RA	Struyf F., Posavac C.M., Keyaerts E., Van Ranst M., Corey L.,			
RT	"Search for polymorphisms in the genes for herpesvirus entry mediator,			
RT	Nectin-1, and Nectin-2 in immune seronegative individuals.";			
RL	J. Infect. Dis. 185:36-44(2002).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Butler K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,			
RA	Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,			

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OY 50 GSECCPKCSPGYRVKAEAGELTGV-----CEPCPG---TYIAHLNGLSKLQCOMCD 100
Db 56 GQFCHKPCPPGGRKARDC-----TVNGDEPDVCVPCOEGKEYTDKAFS--SKRCRCRLCD 108
OY 101 PAMGLRASRNCSTENAVCGSPGHFCIVQDGDHCAACRAVATSSPGQRVQKGTESQDT 160
Db 109 EGHGLEVEINCTRTONTKCRCKNFFC-----NST 138
OY 161 LCQNCPPGTFSFNGTLEEC--QHQTCSMLVTKAGAGTSSSHWWMFLSGSLVIIVICST 218
Db 139 VCEHCDPCTKCEHGIKECTILTSNTKC-----KEGSRSNLGM-----LCLLLLP 183
OY 219 VGLICVRRKPRGDDVIVIVSVQKROEAGEATVIEALQAPPDVTVAVEETIPSEFTG 278
Db 184 IPLIWMVRKE-----VQKCRKHKRKENQGSHEPTLNPETVAIVLSDVDLSKYITTYIAG 238
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Search completed: November 14, 2003, 17:32:18
Job time : 22 secs

Db 71 TSDTVACDCEASMYTQVMNQFRTCLSSCSSCTTDQVEIRA---CTKQNRVCACGAGRYC 127
 QY 128 IYD-DGDHCAACRAVYATSSGQRYQKGTESQDTLCQNCPPGTF--PNGTLECCQHTQC 185
 Db 128 ALKTHSGSROCKRLKCGPGFVNASRPAENGVLCKACAPGTFSDTSDVCRPHRIC 187
 QY 186 SMLVTKAGAGTSS 198
 Db 188 SIIAIPGNASTDA 200

RESULT 13

148854

gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)

C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
 C/Accession: 148854
 R/Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
 Mamm. Genome 5, 726-727, 1994
 A/Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
 A/Reference number: 148854; MUID:95178848; PMID:7873884
 A/Accession: 148854
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-459 <RES>

A/Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
 C/Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 F:/151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 13.5%; Score 212.5; DB 2; Length 459;
 Best Local Similarity 30.9%; Pred. No. 2,8e-08;

Matches 46; Conservative 18; Mismatches 80; Indels 5; Gaps 4;

QY 53 CCEKCSGPRVKAACGELTGTCPCPPGTYYAHNLGSLKLCQC-QMCDPAMGLRASRNC 111
 Db 39 CCAKCPGQYVKHFKCNKTSPTVCADCEASMYTQVMNQFRTCLSSCSSC--STDQVETRAC 96
 QY 112 SRPENAIVCGSPHFCTIQ-DGDHCAACRAVYATSSGQRYQKGTESQDTLCQNCPPGTF 170
 Db 97 TKQNRVVCACGAGRYQKALKTHSGSCRCQKMLSKCGFGVASSRAPNGVLCKACAPGTF 156
 QY 171 S-PNGTLECCQHTQCSMLVTKAGAGTSS 198
 Db 157 SDTTSSTDVCRPHRICSIIPAENASTDA 185

RESULT 14

JC2395

Fas antigen precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999

C/Accession: JC2395; PC2246

R/Kimura, K.; Wakatsuki, T.; Yamamoto, M.

Biochem. Biophys. Res. Commun. 198, 666-674, 1994

A/Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver

A/Reference number: JC2395; MUID:94128114; PMID:7507668

A/Accession: JC2395

A/Molecule type: mRNA

A/Residues: 1-324 <KIM>

A/Cross-references: DDBJ:D26112; NID:g468486; PIDN:BA05108.1; PID:d1005650; PID:g468487

A/Experimental source: thymus

A/Accession: PC2246

A/Molecule type: mRNA

A/Residues: 1-62, 'RPT' <K12>

A/Cross-references: DDBJ:D26113; NID:g468488; PIDN:BA05109.1; PID:d1005651; PID:g468489

A/Experimental source: liver

C/Genetics: 62/1

A/Intons: 62/1

C/Superfamily: NGF receptor repeat homology

C/Keywords: transmembrane protein

F:/1-21/Domain: signal sequence #status predicted <SIG>

F:/22-324/Product: Fas antigen #status predicted <MAT>

F:/4-79/Domain: NGF receptor repeat homology <NGF>

F:/81-124/Domain: NGF receptor repeat homology <NGA>
 F:/171-186/Domain: transmembrane #status predicted <TM>

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 Best Local Similarity 24.7%; Pred. No. 5.7e-08;

Matches 58; Conservative 27; Mismatches 93; Indels 57; Gaps 6;

QY 41 SCKEDBYPGSECCCKSPGVRVKAACGELTGT-VCEPPPG-TYIAHLNGSLKLCQCM 98
 Db 43 NCSBGLYGVPCPCQPCQGERKVKDCTTSGGAPFCHPCTCEBEYDRKHYDKCRCAF 102
 QY 99 CDPAMGLRASRNCSTENAVCGSPGHFCTIVDGDHCAACRAVYATSSPGQRYQKGTESQ 158
 Db 103 CDEGHLEVENCTRTQNTKCRCKENFYCNALCHCHYHC-----TSCGLEDILPEPTRS 158
 QY 159 DPLCQNCPPGTPSPNGTLECCQHTKCSMLVTKAGAGTSSSHWVWFLSGSLVIYVCT 218
 Db 159 NTRCKK-----QSSNYKLMIL-----ILPGL 180
 QY 219 VGLIICVRRKRGDVVKVIVSVORRQBEAGATYIALQAPDVTVAVEETI 273
 Db 181 AILFVFIYR-----YRKROPDESGIPSEVPMNVSDVNLKTYI 222

RESULT 15

A40036

apoptosis-mediating surface antigen Fas precursor - human

N/Alternate names: surface antigen APO-1

C/Species: Homo sapiens (man)

C/Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000

C/Accession: A40036; S24543; A38142

R/Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Samehima, M.; Hase,

Cell 66, 233-243, 1991

A/Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can med.

A/Reference number: A40036; MUID:91309137; PMID:1713127

A/Accession: A40036

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-335 <ITO>

A/Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410

R/Kramer, P.H.

submitted to the EMBL Data Library, February 1992

A/Reference number: S24543

A/Accession: S24543

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-335 <KRA>

A/Cross-references: EMBL:X63717; NID:g28741; PID:g28742

R/Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Rict

J. Biol. Chem. 267, 10709-10715, 1992

A/Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member

A/Reference number: A38142; MUID:92268122; PMID:1375228

A/Accession: A38142

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-134, 'Q', 136-335 <OEH>

A/Experimental source: SKW6.4 cells

A/Note: sequence extracted from NCBI backbone (NCBIP:103810)

A/Note: in NCBI backbone the source is designated as mouse

C/Genetics:

A/Gene: GDB:APT1

A/Cross-references: GDB:132671; OMIM:134637

A/Map position: 10q24.1-10q24.1

C/Superfamily: NGF receptor repeat homology

C/Keywords: apoptosis; surface antigen; transmembrane protein

F:/1-16/Domain: signal sequence #status predicted <SIG>

F:/85-128/Domain: NGF receptor repeat homology <NGA>

F:/174-190/Domain: transmembrane #status predicted <TM>

Query Match 13.1%; Score 206; DB 2; Length 335;
 Best Local Similarity 25.0%; Pred. No. 6.4e-08;
 Matches 60; Conservative 30; Mismatches 82; Indels 68; Gaps 9;

OY 161 LCQNCPPGTSPPNGTLEECQHQTCKS 186
 Db 122 -CVPCCPGHSP-GSNQACKPWTNCT 145

RESULT 10

GOVZML

T2 protein - myxoma virus (strain Lausanne)
 C/Species: myxoma virus
 C/Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
 C/Accession: A40566
 R/Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
 Virolgy 184, 370-382, 1991
 A/Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor
 A/Reference number: A40566; MUID:91335768; PMID:1651597
 A/Accession: A40566
 A/Molecule type: DNA
 A/Residues: 1-326 <UNT>
 A/Cross-references: GB:M95181; GB:M37976; NID:9332309; PIDN:AAA46632.1; PID:9332310
 C/Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
 C/Keywords: glycoprotein
 F/64-105/Domain: NGF receptor repeat homology <NG2>
 F/106-147/Domain: NGF receptor repeat homology <NG3>
 F/66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.1%; Score 238.5; DB 1; Length 326;
 Best Local Similarity 26.8%; Pred. No. 2,7e-10;
 Matches 73; Conservative 30; Mismatches 104; Indels 65; Gaps 11;

OY 20 VLRLVLYTLF-----GAPCYALPSPCKEDYPVSGCCPKSPGYRVKACGELTGT 73
 Db 1 MFRLLTLAVAVCYVGGAP-YGADRGRKGRNDYKDGICTSCPPGSAVRLCGPSDR 59
 OY 74 VCEPCPGTYIAHLNGLSKLQCC-MCDPMAGLARSNCSTENAVGCCSPGHCTVODG 132
 Db 60 VCSCKKIEFTASTNHAPACVSCRGRC--TSHLESOSCDTRRVCDSCAGNYCLKQ 117
 OY 133 DHCAACRAVATSSPGQVQKGTSSODTLCONCPPTGFPN-GLTECO-----180
 Db 118 EGGIC-APKTKCAGVGSHTRTGVLCTKCRITYSDAVSTETCTSSFNISVEFN 176
 OY 181 ---HQTCKSWLVTKAG-----GTSSSHWVWPLSGS 209
 Db 177 LYPNDITSCT---TTAGNENVVKTSEFVTLNHTDCDPVFTREYYGTSGSGAGGFTGM 233
 OY 210 ---LVIVYGVSTGLIICVRRKRKRDVVKYI 238
 Db 234 DRYONTTKMCTLNIEIRCV-----GDAVRTI 260

RESULT 11

148700

gene OX40 protein - mouse
 N/Alternate names: OX40 antigen
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
 C/Accession: I48700; I48334; S34377
 R/Caldrehead, D.M.; Buhlmann, J.E.; van den Beertwegh, A.J.; Claassen, E.; Noelle, R.J.;
 J. Immunol. 151, 5261-5271, 1993
 A/Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell int
 A/Reference number: I48700; MUID:94044750; PMID:8228223
 A/Accession: I48700
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-272 <RES>
 A/Cross-references: EMBL:Z21674; NID:9312827; PIDN:CAA79772.1; PID:9312828
 R/Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
 Eur. J. Immunol. 25, 926-930, 1995
 A/Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
 A/Reference number: I48334; MUID:95255413; PMID:7737295
 A/Accession: I48334
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA

A/Residues: 1-14, 'G', 16-272 <RE2>
 A/Cross-references: EMBL:X85214; NID:9732818; PIDN:CAA9476.1; PID:9732819
 C/Genetics:
 A/Gene: OX40
 A/Insertions: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
 C/Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 13.7%; Score 215.5; DB 2; Length 272;
 Best Local Similarity 31.5%; Pred. No. 1,1e-08;
 Matches 46; Conservative 17; Mismatches 58; Indels 25; Gaps 5;

OY 41 SCDEYPVSGCCPKSPGYRVKACGELTGVCEPCPGTYIAHLNGLSKLQCCMCD 100
 Db 26 NCVGHYTPSGHKCCRECPGHWVSRCDHRTDLCHPCEFGFYEAVN-YDTCKQCTQCN 84
 OY 101 PANGLRASRNCSTENAVGCCSPGHCTVODGSHCAACRAVATSSPGQVQKGTESQDT 160
 Db 85 HRSSELKQNTCTPQDVTVCRCRPG-----TQP--RQDSGYKGLVD- 122
 OY 161 LCQNCPPGTSPPNGTLEECQHQTCKS 186
 Db 123 -CVPCCPGHSP-GNNQACKPWTNCT 146

RESULT 12

B38634

tumor necrosis factor receptor type 2 precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
 C/Accession: B38634; A40254; S54816
 R/Lewis, M.; Tarragila, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
 A/Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
 A/Reference number: A38634; MUID:9187885; PMID:1849278
 A/Accession: B38634
 A/Molecule type: mRNA
 A/Residues: 1-474 <LEM>
 A/Cross-references: GB:M60469; NID:919827; PIDN:AAA39752.1; PID:919828
 R/Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jen
 Mol. Cell. Biol. 11, 3020-3026, 1991
 A/Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
 A/Reference number: A40254; MUID:91246168; PMID:1645445
 A/Accession: A40254
 A/Molecule type: mRNA
 A/Residues: 1-474 <GOO>
 A/Cross-references: GB:M60469; NID:919827; PIDN:AAA39752.1; PID:919828
 R/Kisonegishi, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
 submitted to the EMBL Data Library, May 1995
 A/Description: Characterization of the promoter region of the murine p75-TNF receptor.
 A/Reference number: S54816
 A/Accession: S54816
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-22 <KIS>
 A/Cross-references: EMBL:X87128; NID:9809043; PIDN:CAA6018.1; PID:9809044
 C/Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C/Keywords: cytokine receptor; transmembrane protein
 F/122/Domain: signal sequence #status predicted <SIG>
 F/23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
 F/40-77/Domain: NGF receptor repeat homology <NG1>
 F/79-120/Domain: NGF receptor repeat homology <NG2>
 F/166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 13.5%; Score 213.5; DB 2; Length 474;
 Best Local Similarity 28.5%; Pred. No. 2,4e-08;
 Matches 55; Conservative 20; Mismatches 101; Indels 17; Gaps 6;

OY 20 VLRLVLYTLFAPCAPLPSPCKEDY--PVGSF-----CCKKSPGYRVKACGE 69
 Db 11 VEFQLMAYGHTVPAQVVLTPYKPEGYEQISQEYDRKAQWCKKCPGQYVXHFCK 70
 OY 70 LNTGVCPCPGTYIAHLNGLSKLQCC--QMCDPAMGLASRNCSTENAVGCCSPGHCT 127


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RESULT 7
D36858
gene G4R protein - variola virus
M/Alternate names: B28R protein (COP)
C/Species: variola virus
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
A/Accession: D36858; S46888; S32385; S35987
R: Blinov, V.M.
submitted to GenBank, November 1992
A/Reference number: A36859
A/Accession: D36858
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-349 <BLU>
A/Cross-references: GB:X69198; NID:9456758; PIDN:CAA9137.1; PID:9457087
A/Experimental source: strain India-1967, ssp. major, isolate Ind3
R: Kolykhlov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Froil
submitted to the EMBL Data Library, April 1992
A/Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A/Reference number: S46868
A/Accession: S46868
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-349 <KOL>
A/Cross-references: EMBL:X67117; NID:9516428; PIDN:CAA47540.1; PID:9516449
A/Experimental source: strain India-1967, isolate Ind3
R: Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A/Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A/Reference number: S32385; MUID:93202281; PMID:8384129
A/Accession: S32385
A/Molecule type: DNA
A/Residues: 31-168 <SHC>
A/Cross-references: EMBL:X69198
A/Experimental source: strain India-1967, ssp. major
C/Genetics:
A/Gene: G4R
C/Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F:32-66/Domain: NGF receptor repeat homology <NGF>
F:68-109/Domain: NGF receptor repeat homology <NGF>
F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match
Best Local Similarity 29.3%; Score 257; DB 2; Length 349;
Matches 66; Conservative 23; Mismatches 94; Indels 42; Gaps 8;

QY 21 LRLVLYLPLGAPC-----YAPALPSCKEDYPPVSECPKSPGYEVKACGEL 70
DB 1 KMSVLYLYLPLSCIIINGRDAAPYPPNGKCKDTEYKRNLCCLSCPPGTVAASRLCDSE 60
QY 71 TGTVEPCPPGTIYIAHLNLSKLCLOQ-MCDPAMGLRASRNCSTRENACVCGSPGHFCLV 129
DB 61 TWTQCTPCSGGTFTSRNNHLPACLSGNGRCN--SNQVETRSCNTTHNRICECSPGYCYL 118
QY 130 QGDHCAACRAVATSPGQVQKGGESQDTLCONCPPTFS-----PNGTLE 177
DB 119 KSSSGCKACVSQTKCGIGV-SGHTSVQDVLCSPGFGTTHYVSSAKCEPVPNNNTN 177
QY 178 ECQ-----HQTCKSMLVYTAGAGTSSSHWWMFLSGSLVI 214
DB 178 YIDVEITLVVNDTSCRTT---TGLSES-----ILTSELTITM 214

RESULT 8
154182
tumor necrosis factor receptor 2-related protein - human
C/Species: Homo sapiens (man)
C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
A/Accession: I54182
R: Baens, M.; Chalfanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A/Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A/Reference number: I54182; MUID:93252381; PMID:8486360

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A/Accession: I54182
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-435 <RES>
A/Cross-references: GB:L04270; NID:9339761; PIDN:AAA36757.1; PID:9339762
C/Genetics:
A/Gene: GDB: LTR8
A/Cross-references: GDB:1230195; OMIM:600979
A/Map position: 12p13.3-12p13.1
C/Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match
Best Local Similarity 16.0%; Score 253; DB 2; Length 435;
Matches 86; Conservative 37; Mismatches 127; Indels 72; Gaps 16;

QY 4 PG-DMGPPPMSTPTDVLRLVLYLFL-----GACVAPALPSCK--EDFY--PQGS 51
DB 10 PGLAMGP-----LVLLGLFGLAASQPAVPVASENQTCDROEKEXYEPQHR 56
QY 52 ECCPCSPGYRVKACGELGTVCPCPPGTIYIAHLNLSKLCLOCOMCDPAMGLASRNC 111
DB 57 ICCSRCPPGTYVSAKCSIRDTVCATCAENSYNEHWNTLTICLCRPPCDPVWGLEIAPC 116
QY 112 SRTENAVCGSPGHFICIVQDGDHCAACRAVATSSPG-----QVQKGTESQDTLCONC 165
DB 117 TSKRKTQCRQCPGMFCAMW-ALECHHCLLSDCPPGTEBELKDEYKGNH-----CVPC 170
QY 166 PPGTF---SPNGTLEBCQHOTKC-SWLVTAGACTSSSHWWM-----FLSGSLVI 212
DB 171 KAGHPQNTSPSPA--RCQPHTRCENQGLVEAPTAQSDTCKNPLERLPPEMSGTMM 227
QY 213 VIVCTVGLII-----CVKRRKRGVNVVYVQKROAEAGETVIEALQAP---- 261
DB 228 LAVLLPLAFPLLATVFSCTIWKSHD--SLCKRLGSLKRRPGGSPVPAVGSWEPPKAP 285
QY 262 --PDVTVAVETIPIPSFTGRSP 281
DB 286 YFPDL-----VQPLPLPSGDVSP 303

RESULT 9
S12783
OX40 antigen precursor - rat
M/Alternate names: nerve growth factor receptor homolog
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
A/Accession: S12783; S08036
R: Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A/Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte
A/Reference number: S12783; MUID:90214614; PMID:2157591
A/Accession: S12783
A/Molecule type: mRNA
A/Residues: 1-271 <MAL>
A/Cross-references: EMBL:X17037; NID:9578330; PIDN:CAA34897.1; PID:9578331
C/Superfamily: CD27 antigen; NGF receptor repeat homology
C/Keywords: growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-271/Product: OX40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match
Best Local Similarity 15.2%; Score 240.5; DB 2; Length 271;
Matches 51; Conservative 16; Mismatches 54; Indels 25; Gaps 5;

QY 41 SCKEDYFVSGBCPKSPGYRVKACGELGTVCPCPPGTIYIAHLNLSKLCLOCOMCD 100
DB 25 NCVQDTYVSGHKKCEQCPGHGMVSRCHNTDVTCHPEPGRYNAVN-YDTCXQCTQCN 83
QY 101 PAMGLASRNCSTRENACVCGSPGHFICIVQDGDHCAACRAVATSSPGQVQKGTESQDT 160
DB 84 HRSGELQONCTPEDTVCOCRPG--TOPRQDSH-----KLGVN----- 121

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A:Reference number: A36007; MUID:90349572; PMID:2166946
A:Accession: A36007
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140 'P',142-195 'R',197-362 'T',364-461 <HEL>
A:Cross-references: GB:M35857; NID:9339751; PIDN:AAA6362.1; PID:9339752
R:Loetscher, H.; Schlaefer, E.C.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors
A:Reference number: A23666; MUID:91056048; PMID:2173696
A:Accession: A23666
A:Status: preliminary
A:Molecule type: protein
A:Residues: 23-40;65-69;136-141;300-306 <LOE>
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 15311-15316, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for two distinct receptors
A:Reference number: A35010; MUID:90110215; PMID:2153136
A:Accession: B35010
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-31 <ENG>
R:Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of the human TNF receptor
A:Reference number: I38094; MUID:95121934; PMID:7821811
A:Accession: I38094
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:9825701
C:Genetics:
A:Gene: GDB:TNFR2
A:Cross-references: GDB:125914; OMIM:191191
A:Map position: 1p36.2-1p36.2
A:Intons: 26/3
A:Note: the list of introns is incomplete
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:22-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F:40-76/Domain: NGF receptor repeat homology <NG1>
F:78-119/Domain: NGF receptor repeat homology <NG2>
F:120-162/Domain: NGF receptor repeat homology <NG3>
F:164-201/Domain: NGF receptor repeat homology <NG4>
F:262-379/Domain: transmembrane #status predicted <TMN>
F:280-461/Domain: intracellular #status predicted <INT>
F:111/193/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 16.4%; Score 259; DB 1; Length 461;
Best Local Similarity 32.8%; Pred. No. 1.1e-11;
Matches 59; Conservative 23; Mismatches 76; Indels 22; Gaps 6;

QY 35 YAPALPS-CRDEY--EVSGECPCPKSPGYRVKACGELTGTVCPCPGTYIAHLNGLS 91
Db 32 YAPPGSTCRRLREYDQTAQWCKSCSPGQAKVFCRTKSDTVCDSCDSEDTYQJMWVP 91
QY 92 KCIQCQCMCDPAMGLRARN-----CSTENAVGCGSPGHFCTVQDDDHCAACRAVATSS 145
Db 92 ECLISC-----GSRCSDDVETQACTREONRITCTCRPGWYCALSKQEGRLCAPLRKR 144
QY 146 PGQVQKGTGTSQDTLQNCPCPGTFS--PNCGLTCCQHTQKCSMLVTAKAG-----TSSS 199
Db 145 PGQVAVRPGTETISIVVCKPAPGTFSTNTSSTDICRHOICNVVAIFGNASMAVCTSTS 204

RESULT 5
T28623
hypothetical protein G2R - variola major virus
C/Species: variola major virus
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C/Accession: T28623
R/Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Uterback, T.R.; Knight, J.C.; Aubin

Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
A:Reference number: Z20488; MUID:94088747; PMID:8264798
A:Accession: T28623
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-348 <NAS>
A:Cross-references: EMBL:L22579; NID:9623595; PIDN:AAA60933.1; PID:9439102
A:Experimental source: strain Bangladesh 1975
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 16.3%; Score 257.5; DB 2; Length 348;
Best Local Similarity 29.5%; Pred. No. 1.2e-11;
Matches 66; Conservative 23; Mismatches 94; Indels 41; Gaps 8;

QY 21 LRLVLYTLFLGAPC-----YAPALPSCKDEYEVSGECPCPKSPGYRVKACGELT 71
Db 1 MKSVLYLYTLFLSCITINGRDADPYTPNGCKDTEYKRNHLCCLSCPGTYASRLCDSKT 60
QY 72 GTVCEPCPGTYIAHLNGLSKLQCO-MCDPAMGLRARNCRSTENAVGCGSPGHFCTVQ 130
Db 61 NTQCTPCGSGTFTSRNNHLPACLSGRCN--SNQVETRSCHTNRICGSGYCLL 118
QY 131 DGDHCAACRAVATSSPGQVQKGTGTSQDTLQNCPCPGTFS-----PNCGLTLE 178
Db 119 GSSGCKACVSGTKGIGYGV-SGHTSVGVIVCSPCGFGTYSHTVSSADKCEPVPNNTFNY 177
QY 179 CQ-----HOTKCSMLVTAKAGTSSSHWMMFLSGSLVTVI 214
Db 178 IDVEITLYPVNDTSCTRTT--TGLSES-----ILTSELTITM 213

RESULT 6
D27175
G2R protein - variola minor virus (strain Garcia-1966)
C/Species: variola minor virus
C/Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C/Accession: D72175
R:Shchelkunov, S.N.; Tolmenin, A.V.; Gucorov, V.V.; Safonov, P.F.; Massung, R.F.; Lopa
submitted to Genbank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: D72175
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1348 <SHC>
A:Cross-references: GB:Y16780; NID:95830555; PIDN:CAB54798.1; PID:95830759
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: G2R
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 16.3%; Score 257; DB 2; Length 349;
Best Local Similarity 29.3%; Pred. No. 1.3e-11;
Matches 66; Conservative 23; Mismatches 94; Indels 42; Gaps 8;

QY 21 LRLVLYTLFLGAPC-----YAPALPSCKDEYEVSGECPCPKSPGYRVKACGELT 70
Db 1 MKSVLYLYTLFLSCITINGRDADPYTPNGCKDTEYKRNHLCCLSCPGTYASRLCDSK 60
QY 71 TGVCEPCPGTYIAHLNGLSKLQCO-MCDPAMGLRARNCRSTENAVGCGSPGHFCTV 129
Db 61 TNGCTPCGSGTFTSRNNHLPACLSGRCN--SNQVETRSCHTNRICGSGYCLL 118
QY 130 QDGDHCAACRAVATSSPGQVQKGTGTSQDTLQNCPCPGTFS-----PNCGLTLE 177
Db 119 KSSGCKACVSGTKGIGYGV-SGHTSVGVIVCSPCGFGTYSHTVSSADKCEPVPNNTFN 177
QY 178 ECQ-----HOTKCSMLVTAKAGTSSSHWMMFLSGSLVTVI 214
Db 178 YIDVEITLYPVNDTSCTRTT--TGLSES-----ILTSELTITM 214

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RESULT 15

AA05797 standard; Protein; 283 AA.

XX AA05797;

XX 02-AUG-1999 (first entry)

XX Herpes virus entry mediator (HVEM).

XX Herpes virus entry mediator; HVEM; HSV receptor; infection;

XX diagnosis; therapy; vaccine; antiviral; assay.

XX Human herpes simplex virus.

XX WO9920761-A2.

XX 29-APR-1999.

XX 22-OCT-1998; 98WO-US22342.

XX 22-OCT-1997; 97US-0955531.

XX (UNMI) UNIV MICHIGAN.

XX Fuller AO, Li Q, McLaren NC, Perez A, Subramanian G;

XX WPI: 1999-302740/25.

XX N-PSDB; AAX25512.

XX Human herpes simplex virus receptor B5 and HVEM compositions

XX Claim 10; Page 71-72; 89pp; English.

XX The present sequence represents HVEM, a novel human herpes simplex virus (HSV) entry mediator that is a member of the tumour necrosis factor receptor family, and which confers on HSV the ability to infect and replicate in otherwise non-permissive cells. In the CC present invention, the combination of a novel porcine cell model CC system which is refractory to HCV entry, along with specific HSV B5 CC (see AA05796) and/or HVEM receptor proteins enables the development CC of assays for screening antiviral compounds and therapeutics. The CC assays are useful for detecting the ability of agents to inhibit CC HSV entry or spread and provide for facile high-throughput CC screening of compounds suspected to be able to inhibit such entry, CC e.g. compound libraries, peptide libraries etc., to identify CC potential drug candidates. The invention also provides a vaccine CC comprising the HSV receptor, an immunogenic polypeptide or CC fragments of the polypeptide.

SQ Sequence 283 AA;

Query Match 99.5%; Score 1570; DB 20; Length 283;

Best Local Similarity 99.3%; Pred. No. 5.9e-120; Mismatches 281; Conservative 1; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDYVPGSECCPKCSRG 60
DB 1 MEPPGDMGPPWRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDYVPGSECCPKCSPG 60
QY 61 YRVKACGELTGTVCPCPCTYIAHLNGLSKLCQCOMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCPCPCTYIAHLNGLSKLCQCOMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVDDGHCACRAVATSSPGQVQKGTESQDTLCQNCPPGTSPNGTLEECQ 180
DB 121 CSPGHFCIVDDGHCACRAVATSSPGQVQKGTESQDTLCQNCPPGTSPNGTLEECQ 180
QY 181 HQTKCSWLVTYKAGAGTSSHWMMFLSGSLVIVIVCSTVGLITCVKRRKPRGDVVKIVS 240
DB 181 HQTKCSWLVTYKAGAGTSSHWMMFLSGSLVIVIVCSTVGLITCVKRRKPRGDVVKIVS 240

QY 241 VQRKQAEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
DB 241 VQRKQAEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

Search completed: November 14, 2003, 17:30:21
Job time : 42 secs

PT useful for treating stroke, Alzheimer's disease and AIDS
 XX
 PS Disclosure; Page 13-14; 18pp; English.
 CC The invention relates to identifying agonists or antagonists to tumour
 CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TR2
 CC and TR4). The method comprises: (a) (i) contacting TR1 or TR2 with a
 CC candidate compound in the presence of TR2 or TR4; or (ii) contacting TR2
 CC or TR4 with a candidate compound in the presence of TR1 or TR2; and (b)
 CC assessing the ability of the candidate compound to compete with TR1 or
 CC TR2 binding to TR2 or TR4. TR and TR agonists and antagonists are useful
 CC for treating diseases caused by imbalance of TR or TR polypeptide levels,
 CC which cause: chronic and acute inflammation, arthritis, septicemia,
 CC autoimmune diseases, transplant rejection, graft vs. host disease,
 CC infection, stroke, ischemia, acute respiratory disease syndrome,
 CC restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis
 CC and Alzheimer's disease. The present sequence represents a TNF-R related
 CC polypeptide TR2.
 CC
 SQ Sequence 283 AA:
 Query Match 99.6%; Score 1572; DB 20; Length 283;
 Best Local Similarity 99.6%; Pred. No. 4.1e-120;
 Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MEPPGDMGPPPPRSTRTDVLRLVLTFLGAPCYAPALPCKEDPYGSSCCPKCSFG 60
 DB 1 MEPPGDMGPPPPRSTRTDVLRLVLTFLGAPCYAPALPCKEDPYGSSCCPKCSFG 60
 QY 61 YVKEACGELTGTCPCPGTYIAHLNGLSKLCOCQCDPAMGLRASNCRSTENAVCG 120
 DB 61 YVKEACGELTGTCPCPGTYIAHLNGLSKLCOCQCDPAMGLRASNCRSTENAVCG 120
 QY 121 CSPGHFCTIVQDDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEBCQ 180
 DB 121 CSPGHFCTIVQDDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEBCQ 180
 QY 181 HOTKCSMLVTXKAGAGTSSSHWWMFLSGSLVIVIVCSITGLIICVRRKPRGDVVKVIVS 240
 DB 181 HOTKCSMLVTXKAGAGTSSSHWWMFLSGSLVIVIVCSITGLIICVRRKPRGDVVKVIVS 240
 QY 241 VORRQOEAEGEATVIEALQAPDVTVAVEETIPSTGSPNH 283
 DB 241 VORRQOEAEGEATVIEALQAPDVTVAVEETIPSTGSPNH 283
 RESULT 14
 AAM12659
 ID AAM12659 standard; Protein; 283 AA.
 AC AAM12659;
 XX
 DT 07-MAY-1997 (first entry)
 XX
 DE Human herpes simplex virus cellular mediator.
 XX
 KW Herpes simplex virus cellular mediator; HVEM; receptor; HSV;
 XX diagnosis; agonist; antagonist; antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..38
 FT /label= Sig_peptide
 FT Protein 39..283
 FT /label= Mat_protein
 FT Region 42..75
 FT /note= "cysteine-rich repeat characteristic of
 FT TNF/NGF receptor family"
 FT Region 76..120
 FT /note= "cysteine-rich repeat characteristic of
 FT TNF/NGF receptor family"
 FT Region 121..162

FT /note= "cysteine-rich repeat characteristic of
 FT TNF/NGF receptor family"
 FT Region 163..185
 FT /note= "partial cysteine-rich repeat characteristic
 FT of TNF/NGF receptor family"
 FT Domain 203..225
 FT /label= Transmembrane_domain
 FT Modified-site 110..112
 FT /label= Glycosylation
 FT /note= "potential N-glycosylation site"
 FT Modified-site 173..175
 FT /label= Glycosylation
 FT /note= "potential N-glycosylation site"
 PN MO9704658-A1.
 XX
 PD 13-FEB-1997.
 XX
 PF 26-JUL-1996; 96WO-US12374.
 XX
 PR 28-JUL-1995; 95US-0509024.
 XX
 PA (NOUN) UNIV NORTHWESTERN.
 XX
 PI Montgomery RI, Spear PG;
 XX
 DR WPI, 1997-145273/13.
 XX
 DR N-PSDB; AAT51737.
 XX
 PT New human herpes simplex virus cellular mediator - used for
 PT diagnosis, drug screening and therapeutically to inhibit entry of
 PT HSV into cells
 XX
 PS Claim 1; Fig 2; 54pp; English.
 XX
 CC Human herpes simplex virus (HSV) cellular mediator (HVEM) (AAM12659)
 CC is a novel member of the TNF/NGF receptor family that mediates or
 CC enhances entry of HSV into cells. Its amino acid sequence was
 CC deduced from a cDNA clone (AAT51737) isolated from an HeLa library
 CC by its ability to convert CHO-K1 cells from resistance to
 CC susceptibility to HSV-1 entry. Recombinant HVEM can be produced in
 CC bacterial or mammalian (esp. CHO) cells. It can be used as an
 CC immunosay reagent to detect specific antibodies, to screen for
 CC drugs having an (ant)agonist effect on HSV entry into cells, to
 CC generate antibodies, to screen for the (currently unknown) HVEM
 CC ligand, and to identify inhibitors of HSV-HVEM interaction.
 CC
 SQ Sequence 283 AA:
 Query Match 99.5%; Score 1570; DB 18; Length 283;
 Best Local Similarity 99.3%; Pred. No. 5.9e-120;
 Matches 281; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MEPPGDMGPPPPRSTRTDVLRLVLTFLGAPCYAPALPCKEDPYGSSCCPKCSFG 60
 DB 1 MEPPGDMGPPPPRSTRTDVLRLVLTFLGAPCYAPALPCKEDPYGSSCCPKCSFG 60
 QY 61 YVKEACGELTGTCPCPGTYIAHLNGLSKLCOCQCDPAMGLRASNCRSTENAVCG 120
 DB 61 YVKEACGELTGTCPCPGTYIAHLNGLSKLCOCQCDPAMGLRASNCRSTENAVCG 120
 QY 121 CSPGHFCTIVQDDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEBCQ 180
 DB 121 CSPGHFCTIVQDDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEBCQ 180
 QY 181 HOTKCSMLVTXKAGAGTSSSHWWMFLSGSLVIVIVCSITGLIICVRRKPRGDVVKVIVS 240
 DB 181 HOTKCSMLVTXKAGAGTSSSHWWMFLSGSLVIVIVCSITGLIICVRRKPRGDVVKVIVS 240
 QY 241 VORRQOEAEGEATVIEALQAPDVTVAVEETIPSTGSPNH 283
 DB 241 VORRQOEAEGEATVIEALQAPDVTVAVEETIPSTGSPNH 283

AC	AA94717;
XX	
DT	29-JAN-2001 (first entry)
XX	
DE	Human TR2-receptor protein sequence.
XX	
KW	Tumour necrosis factor-receptor related protein; TR2; human; cancer;
KW	chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;
KW	immunodeficiency; metastasis; hemolytic anaemia; asthma; X-linked SCID;
KW	severely combined immunodeficiency; apoptosis inhibition;
XX	Alzheimer's disease; Parkinson's disease; Crohn's disease.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Location/Qualifiers
FT	Peptide
FT	1..36
FT	/note= "Signal peptide"
FT	Protein
FT	37..263
FT	/label= "TR2 receptor"
FT	Domain
FT	37..200
FT	/note= "Extracellular domain"
FT	Domain
FT	201..225
FT	/note= "Transmembrane domain"
FT	Domain
FT	226..283
FT	/note= "Intracellular domain"
XX	
PN	WO200056405-A2.
XX	
PD	28-SEP-2000.
XX	
PF	22-MAR-2000; 2000WO-US07521.
XX	
PR	22-MAR-1999; 99US-0125683.
PR	26-MAR-1999; 99US-0126522.
PR	20-MAY-1999; 99US-0135169.
PR	06-AUG-1999; 99US-0147383.
XX	
PA	(NIJ/) NI J
PA	(ROSE/) ROSEN C A.
PA	(GENT/) GENTZ R L.
XX	
PI	NI J, Rosen CA, Gentz RL;
XX	
DR	WPI; 2000-594519/56.
XX	
DR	N-PSDB; AAA28135.
XX	
PT	Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
PT	and its two splice variants, useful for treating arthritis or
PT	inflammation, cancer (such as follicular lymphomas) and
PT	immunodeficiency disorders -
XX	
PS	Claim 1; Fig 1; 373pp; English.
XX	
CC	This invention relates to an isolated nucleic acid molecule encoding a
CC	human tumor necrosis factor (TNF)-receptor related protein TR2. Included
CC	in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
CC	The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a
CC	member of the TNFR superfamily. The invention includes a method for the
CC	treatment of arthritis or inflammation using an antibody directed against
CC	a fragment of the TR2 protein. TR2 its agonists, antagonists and
CC	antibodies exhibit cytostatic, dermatological, antineoplastic,
CC	immunopressive, antiallergic, antiarthritic, antiaesthetic,
CC	antiinflammatory, neuroprotective, nootropic, antiparkinsonian, and
CC	cerebroprotective activity. The methods are useful for treating arthritis
CC	or inflammation, cancer (such as follicular lymphoma, carcinoma with p53
CC	mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an
CC	immunodeficiency or for enhancing an in vivo leukocyte response to an
CC	antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
CC	preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
CC	dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
CC	inflammatory myopathies) and immunodeficiency disorders (such as severely
CC	combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
CC	disorder, or Nezelof syndrome-combined immunodeficiency with IgS). TR2,

	CC	TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or antagonists are useful for treating or preventing autoimmune diseases and inhibit the growth, progression and/or metastasis of cancers. They are also used to activate, differentiate or proliferate cancerous cells or tissue, and can be used to treat diseases associated with increased cell survival, or the inhibition of apoptosis, e.g. Alzheimer's disease.
	CC	Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful as sources for generating antibodies, as molecular weight markers.
	CC	This sequence represents the TR2 receptor protein of the invention.
	XX	
	SS	Sequence 283 AA;
	SQ	
	Query Match	99.8%; Score 1575; DB 21; Length 283;
	Best Local Similarity	99.6%; Pred. No. 2.3e-120;
	Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Oy	1	MEPPGDWGPPEWRSTPRTDVLRLVLYTLFLGAPCYAPALPSCKEDYVPVSGCCPKCSPG 60
Dd	1	MEPPGDWGPPEWRSTPRTDVLRLVLYTLFLGAPCYAPALPSCKEDYVPVSGCCPKCSPG 60
Oy	61	YRVKACAGELTGIVCEPCPEPTGYIAHLNGLSKLQCCMPAMGLRASRNCRTENAVCG 120
Dd	61	YRVKACAGELTGIVCEPCPEPTGYIAHLNGLSKLQCCMPAMGLRASRNCRTENAVCG 120
Oy	121	CSPHFICIVDDGDHCACRAVAITSSPQRVOKGGBESODTLCONCPGTSPNGTLEECQ 180
Dd	121	CSPHFICIVDDGDHCACRAVAITSSPQRVOKGGBESODTLCONCPGTSPNGTLEECQ 180
Oy	181	HOTKCSMLVTKAGAGTSSSHVMWFLLSGSLVIYVCSTVGILICVKRRKPAGDVVKYIVS 240
Dd	181	HQTCSMLVTKAGAGTSSSHVMWFLLSGSLVIYVCSTVGILICVKRRKPAGDVVKYIVS 240
Oy	241	VORRKQAEAGEATVIEALQAPPDVTIVAVEETIPSTFGRSBNH 283
Dd	241	VORRKQAEAGEATVIEALQAPPDVTIVAVEETIPSTFGRSBNH 283
	RESULT 13	
ID	AAM95031	standard; protein; 283 AA.
AA	AAM95031	
XX	13-MAY-1999	(first entry)
DE	Tumour necrosis factor receptor (TNF-R) related polypeptide TR2.	
XX		
KM	Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis; inflammation; septicemia; autoimmune disease; transplant rejection; graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS; acute respiratory disease syndrome; restenosis; bone disease; cancer; atherosclerosis; Alzheimer's disease.	
XX	Unidentified.	
OS		
XX	EP897114-A2.	
PN		
XX	17-FEB-1999.	
PD		
XX	04-JUN-1998; 98EP-0304424.	
PF		
XX	29-AUG-1997; 97US-0057550.	
PR	13-AUG-1997; 97US-0055513.	
PR	26-AUG-1997; 97US-0056980.	
XX		
PA	(SMIK) SMITHKLIN BEECHAM CORP.	
XX		
PI	Brigham-Durke MR, Young PR;	
DR	WPI; 1999-134308/12.	
XX		
LT	Identifying agonists and antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (TR1, TR2, TL2 and TL4) -	


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FT Domain 201..225
FT /note="Transmembrane domain"
FT 226..283
FT Domain /note="Intracellular domain"
XX WO9818824-A1.
XX PD 07-MAY-1998.
XX PF 30-OCT-1996; 96WO-US18540.
XX PR 30-OCT-1996; 96WO-US18540.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX Genz RL, Hurle MR, Lyn SDP, Ni J, Rosen CA;
XX WPI; 1998-272139/24.
XX N-PSDB; AAV34509.
XX Nucleic acid encoding TR2 tumour necrosis factor family receptor -
XX and its splice variants, useful for diagnosis and treatment of
XX diseases involving abnormal cell survival or death, e.g. herpes
XX simplex infection
XX PS Claim 1; Fig 1; 151pp; English.
XX CC The human tumour necrosis factor (TNF) receptor related protein (TR2) is
XX a member of the TNF family and displays considerable homology to murine
XX CD40. It can be used in soluble forms to treat herpes simplex virus
XX infection and TR2 proteins (or their agonists or antagonists) are used to
XX treat disease associated with aberrant cell survival. Agonists may also
XX be used to protect against the effects of radiation therapy and to
XX stimulate lymphocyte proliferation and differentiation in patients
XX infected by human immune deficiency syndrome.
XX CC Sequence 283 AA:
SQ
Query Match 99.8%; Score 1575; DB 19; Length 283;
Best Local Similarity 99.6%; Pred. No. 2.3e-120;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPPGDMGPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
DB 1 MEPPGDMGPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
QY 61 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCQCDPAMGLRASRNCSTRTENAVCG 120
DB 61 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCQCDPAMGLRASRNCSTRTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQRVQKGTESODTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQRVQKGTESODTLCONCPGTFSPNGTLEECQ 180
QY 121 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCQCDPAMGLRASRNCSTRTENAVCG 120
DB 121 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCQCDPAMGLRASRNCSTRTENAVCG 120
QY 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVYVCSVTGLIICVRRKRPBGDVVAVYS 240
DB 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVYVCSVTGLIICVRRKRPBGDVVAVYS 240
QY 241 VOKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
DB 241 VOKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
RESULT 11
AAW87591
ID AAW87591 standard; Protein; 283 AA.
XX AAW87591;
XX 17-MAR-1999 (first entry)
XX Human tumour necrosis factor receptor-like 2 protein.

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XX XX Tumour necrosis factor receptor-like 2; TR2; TNF; human; psoriasis;
XX systemic lupus erythematosus; idiopathic thrombocytopenic purpura;
XX rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
XX insulin-dependent diabetes mellitus; allergic disorder; cancer; therapy;
XX atherosclerosis; viral infection.
XX OS Homo sapiens.
XX WO9851346-A1.
XX PD 19-NOV-1998.
XX PF 12-MAY-1998; 96WO-US09744.
XX PR 12-MAY-1997; 97US-0046249.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX Harrop JA, Holmes SD, Reddy MP, Truneh A;
XX WPI; 1999-059689/05.
XX N-PSDB; AAV83763.
XX Method of treating pathological condition - comprises administering
XX tumour necrosis factor-2 antibody to patient
XX PS Disclosure; Page 27-28; 35pp; English.
XX CC This sequence represents the human tumour necrosis factor (TNF)
XX receptor-like 2 (TR2) protein. Antibodies that target the TR2 protein can
XX be used in the method of the invention to treat pathological conditions.
XX The method is used to treat systemic lupus erythematosus, idiopathic
XX thrombocytopenic purpura, rheumatoid arthritis, multiple sclerosis,
XX psoriasis, inflammatory bowel disease, insulin-dependent diabetes
XX mellitus, allergic disorders, e.g. asthma, allergic rhinitis and atopic
XX dermatitis, cancer, e.g. lymphomas and leukemias, atherosclerosis and
XX viral infections, e.g. Herpes simplex virus and AIDS. The TR2 antibody
XX is also used to monitor and diagnose abnormalities in TR-2 function,
XX production or metabolism.
XX CC Sequence 283 AA:
SQ
Query Match 99.8%; Score 1575; DB 20; Length 283;
Best Local Similarity 99.6%; Pred. No. 2.3e-120;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPPGDMGPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
DB 1 MEPPGDMGPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
QY 61 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCQCDPAMGLRASRNCSTRTENAVCG 120
DB 61 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCQCDPAMGLRASRNCSTRTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQRVQKGTESODTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQRVQKGTESODTLCONCPGTFSPNGTLEECQ 180
QY 121 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCQCDPAMGLRASRNCSTRTENAVCG 120
DB 121 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCQCDPAMGLRASRNCSTRTENAVCG 120
QY 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVYVCSVTGLIICVRRKRPBGDVVAVYS 240
DB 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVYVCSVTGLIICVRRKRPBGDVVAVYS 240
QY 241 VOKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
DB 241 VOKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
RESULT 12
AA94717
ID AA94717 standard; Protein; 283 AA.
XX AA94717
XX

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Best Local Similarity 100.0%; Pred. No. 1.3e-120; Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMWRSTPTDVLRLVLYLTFGLGAPCYAPALPSCKEDEYVGSCECPKCSFG 60
 Db 1 MEPPGDMGPPMWRSTPTDVLRLVLYLTFGLGAPCYAPALPSCKEDEYVGSCECPKCSFG 60

QY 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
 Db 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120

QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTSPNGTLEECQ 180
 Db 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTSPNGTLEECQ 180

QY 181 HQTKCSMLVTKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKPRGVDVVKYIVS 240
 Db 181 HQTKCSMLVTKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKPRGVDVVKYIVS 240

QY 241 VQRRQBAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283
 Db 241 VQRRQBAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283

RESULT 9
 ID ABU60681 standard; Protein; 283 AA.
 AC ABU60681;
 DT 06-MAY-2003 (first entry)
 DE Human membrane-bound Herpesvirus Entry Mediator (mHEM).

XX Human, receptor; TANGO-69 receptor; herpesvirus entry mediator; HEM;
 KW SHVEM1; SHVEM2; SHVEM3; mHEM2; tumour necrosis factor receptor; TNFR;
 KW immune disorder; autoimmune disorder; arthritis; graft rejection;
 KW T-cell disorder; AIDS; inflammatory disorder; bacterial infection;
 KW psoriasis; septicemia; cerebral malaria; inflammatory bowel disease;
 KW rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;
 KW asthma; psoriasis; apoptotic disorder; rheumatoid arthritis;
 KW systemic lupus erythematosus; insulin-dependent diabetes mellitus;
 KW cytotoxic disorder; septic shock; cachexia; proliferative disorder;
 KW B-cell cancer.

OS Homo sapiens.
 XX US2002132297-A1.
 XX 19-SEP-2002.
 XX 21-AUG-2001; 2001US-0934289.
 XX 03-SEP-1998; 98US-0146950.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Busfield SJ;
 XX WPI; 2003-246556/25.
 XX N-PSDB; ABX90562.
 XX New TANGO-69 receptor polynucleotides and polypeptides, useful for
 PT treating arthritis, graft rejection, AIDS, bacterial infection,
 PT psoriasis, septicemia, cerebral malaria, inflammatory bowel disease,
 PT asthma, psoriasis, lupus
 XX
 PS Disclosure; Fig 10; 79pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule, designated as
 CC TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a
 CC portion of the proteins SHVEM1, SHVEM2, SHVEM3 and mHEM2 (where HEM is
 CC Herpesvirus Entry Mediator and "s" refers to a soluble form and "m" to a

CC membrane bound form). Also included are a host cell containing TANGO-69
 CC receptor nucleic acid, a non-human mammalian host cell containing
 CC TANGO-69 receptor nucleic acid, an isolated polypeptide that is encoded
 CC by TANGO-69 receptor nucleic acid, an antibody that selectively binds to
 CC the TANGO-69 receptor polypeptide, and identifying a compound that binds
 CC to and/or modulates the activity of the TANGO-69 receptor polypeptide.
 CC The polynucleotides, polypeptides compounds and methods are useful for
 CC treating immune disorders such as autoimmune disorders (e.g. arthritis,
 CC graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g.
 CC bacterial infection, psoriasis, septicemia, cerebral malaria
 CC inflammatory bowel disease, rheumatoid arthritis, osteoarthritis),
 CC allergic inflammatory disorders (e.g. asthma, psoriasis),
 CC apoptotic disorders (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, insulin-dependent diabetes mellitus), cytotoxic disorders,
 CC septic shock, cachexia, and proliferative disorders (e.g. B-cell
 CC cancers). TANGO-69 receptor is a member of the TNF (tumour necrosis
 CC factor) superfamily of proteins. The present sequence represents a
 CC TANGO-69 receptor protein.
 CC
 SQ Sequence 283 AA;
 XX

Query Match 100.0%; Score 1578; DB 24; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1.3e-120; Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMWRSTPTDVLRLVLYLTFGLGAPCYAPALPSCKEDEYVGSCECPKCSFG 60
 Db 1 MEPPGDMGPPMWRSTPTDVLRLVLYLTFGLGAPCYAPALPSCKEDEYVGSCECPKCSFG 60

QY 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
 Db 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120

QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTSPNGTLEECQ 180
 Db 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTSPNGTLEECQ 180

QY 181 HQTKCSMLVTKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKPRGVDVVKYIVS 240
 Db 181 HQTKCSMLVTKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKPRGVDVVKYIVS 240

QY 241 VQRRQBAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283
 Db 241 VQRRQBAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283

RESULT 10
 ID AAM60045 standard; Protein; 283 AA.
 AC AAM60045;
 XX 25-SEP-1998 (first entry)
 XX Human TNF receptor related (TR2) protein.
 XX Human, tumour necrosis factor; TNF; herpes simplex virus;
 KW aberrant cell survival; radiation therapy; lymphocyte proliferation;
 KW immune deficiency syndrome.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..36
 FT /note= "Signal peptide"
 FT Peptide 37..283
 FT /note= "Mature peptide"
 FT Domain 37..200
 FT /note= "Extracellular domain"
 FT Modified-site 110
 FT /note= "Asparagine-linked glycosylation site"
 FT Modified-site 173
 FT /note= "Asparagine-linked glycosylation site"

KM Human: tumour necrosis factor receptor; TNFR-6alpha; TNFR-6beta; therapy;
 KM immune system-related disorder; inflammatory disease; immunosuppressive;
 KM bowel disease; encephalitis; atherosclerosis; gastrointestinal Gen;
 KM autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
 KM multiple sclerosis; Crohn's disease; autoimmune encephalitis; allergy;
 KM graft versus host disease; GVHD; anti-inflammatory; psoriasis; arthritis;
 KM neuroprotective; antiarteriosclerotic; dermatological; asthma.
 XX
 OS Homo sapiens.
 XX
 PN WO200218622-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 24-AUG-2001; 2001WO-US26396.
 XX
 PR 25-AUG-2000; 2000US-227598P.
 PR 21-NOV-2000; 2000US-252131P.
 PR 06-JUL-2001; 2001US-303224P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Gentz RL, Ebner R, Yu G, Ruben SM, Ni J, Feng P;
 DR WPI; 2002-281068/32.
 XX
 PT Novel nucleic acid molecules comprising a polynucleotide encoding human
 PT tumor necrosis factor receptor (TNFR)-6alpha and 6beta polypeptides
 PT useful for treating disease e.g. inflammatory and autoimmune disorders
 PT
 XX
 PS Claim 36; Page 346-347; 350pp; English.
 XX
 CC The invention relates to human tumour necrosis factor receptor (TNFR)-
 CC 6alpha and 6beta protein and their corresponding nucleic acids. The
 CC invention provides screening methods for identifying agonists and
 CC antagonists of TNFR-6alpha and 6beta activity. The invention also
 CC provides diagnostic and therapeutic methods for detecting and treating
 CC immune system-related disorders. The method is useful for treating or
 CC preventing an inflammatory disease or disorder selected from bowel
 CC disease, encephalitis, atherosclerosis and psoriasis, an autoimmune
 CC disease or disorder selected from systemic lupus erythematosus,
 CC arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease,
 CC and autoimmune encephalitis, graft versus host disease (GVHD), and an
 CC allergy or asthma. The present sequence is human TNFR-6alpha and TNFR-
 CC 6beta related protein.
 CC
 SQ Sequence 283 AA;
 Query Match 100.0%; Score 1578; DB 23; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1,3e-120; Indels 0; Gaps 0;
 Matches 283; Conservative 0; Mismatches 0;

RESULT 8
 ABR40215
 ID ABR40215 standard; Protein; 283 AA.
 XX
 AC ABR40215;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human cobesin.
 XX
 XX Human; cobesin; lipid partitioning; lipid metabolism; weight reduction;
 KM insulin-like activity; free fatty acid oxidation; anorectic; antilipemic;
 KM antiarteriosclerotic; antidiabetic; hypotensive; immunomodulator;
 KM cytostatic; anti-HIV; antiinflammatory; antidepressant; weight loss;
 KM obesity.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Peptide
 FT 1..38
 FT /label= Signal_peptide
 FT Protein
 FT 39..283
 FT /label= Mature_cobesin
 FT Domain
 FT 39..202
 FT /label= Extracellular_domain
 FT Domain
 FT 203..223
 FT /label= Transmembrane_domain
 FT Domain
 FT 224..283
 FT /label= Intracellular_domain
 XX
 PN WO2003011321-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 29-JUL-2002; 2002WO-1B03408.
 XX
 PR 31-JUL-2001; 2001US-309233P.
 XX
 PA (GSEST) GENSET SA.
 XX
 PI Lucas J, Dialynas D, Briggs K;
 DR WPI: 2003-247866/25.
 DR N-PSDB; ABZ95577.
 XX
 PT Screening for an agonist or an antagonist of cobesin activity, useful
 PT for reducing body mass, maintaining weight loss, or preventing or
 PT treating an obesity-related disease or disorder, e.g. hyperlipidemia,
 PT diabetes or hypertension
 XX
 PS Example 10; Page 34; 37pp; English.
 XX
 CC The invention relates to a novel method for screening for an agonist or
 CC an antagonist of cobesin activity, i.e. lipid partitioning, lipid
 CC metabolism, insulin-like activity, free fatty acid oxidation, or weight
 CC reduction. The method of the invention has anorectic, antilipemic,
 CC antiarteriosclerotic, antidiabetic, hypotensive, immunomodulator,
 CC cytostatic, anti-HIV, antiinflammatory, and antidepressant activity. The
 CC method is useful for screening for an agonist or antagonist of cobesin
 CC activity. The agonists or antagonists are useful for reducing body mass,
 CC maintaining weight loss, preventing or treating an obesity-related
 CC disease or disorder, e.g. hyperlipidemia, atherosclerosis, insulin
 CC resistance, diabetes or hypertension. The compounds are also useful for
 CC increasing body mass or treating disorders associated with excessive
 CC weight loss, e.g. cachexia, cancer-related weight loss, acquired
 CC immunodeficiency syndrome (AIDS)-related weight loss, chronic
 CC inflammatory disease-related weight loss or anorexia. The present
 CC sequence represents the human cobesin of the invention.
 XX
 SQ Sequence 283 AA;
 Query Match 100.0%; Score 1578; DB 24; Length 283;

QY	61	YAVKEACGSLTGTVCPCPGTATIAHLNGSLKLOCOMCPDPAKGLASRNCSTENAVG	120
Db	61	YAVKEACGSLTGTVCPCPGTATIAHLNGSLKLOCOMCPDPAKGLASRNCSTENAVG <td>120</td>	120
QY	121	CSPGHFCITQDDGDHCAACRAVATSSPGORVQKGTESODTLCONCPGTFSPGTLEECQ	180
Db	121	CSPGHFCITQDDGDHCAACRAVATSSPGORVQKGTESODTLCONCPGTFSPGTLEECQ	180
QY	181	HOTKCSMLVTKAGAGTSSSHWWWELSGSLVIVICSTVGLIICVRRKRGDVKVIVS	240
Db	181	HOTKCSMLVTKAGAGTSSSHWWWELSGSLVIVICSTVGLIICVRRKRGDVKVIVS	240
QY	241	VORKROEAGEATVIEALQAPDVTVAVEETIPSEFGSPNH	283
Db	241	VORKROEAGEATVIEALQAPDVTVAVEETIPSEFGSPNH	283
RESULT 6			
AAV95348			
ID	AAV95348	standard; Protein; 283 AA.	
XX	AAV95348;		
XX	25-SEP-2000	(first entry)	
XX	Human PRO509 antitumour protein.		
XX	PRO509; human; antitumour; tumour; therapy; cytostatic;		
KW	breast cancer; ovarian cancer; renal cancer; colorectal cancer;		
KW	uterine cancer; prostate cancer; lung cancer; bladder cancer;		
KW	central nervous system cancer; melanoma; leukaemia; neoplasm.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FH	Peptide	1..36	
FT	Protein	/label= Signal_peptide	
FT	Domain	37..283	
FT		/label= PRO509	
FT	Modified-site	205..221	
FT		/note= "transmembrane domain"	
FT	Modified-site	81..87	
FT		/note= "N-myristoylation"	
FT	Modified-site	89..95	
FT		/note= "N-myristoylation"	
FT	Modified-site	104..110	
FT		/note= "N-myristoylation"	
FT	Modified-site	120..126	
FT		/note= "N-myristoylation"	
FT	Modified-site	153..159	
FT		/note= "N-myristoylation"	
FT	Modified-site	193..199	
FT		/note= "N-myristoylation"	
FT	Modified-site	192..201	
FT		/note= "N-myristoylation"	
FT	Modified-site	220..226	
FT		/note= "N-myristoylation"	
FT	Modified-site	110..114	
FT		/note= "Asn is N-glycosylated"	
FT	Modified-site	173..177	
FT		/note= "Asn is N-glycosylated"	
FT	Region	231..234	
FT		/note= "cell attachment sequence"	
XX	WO200037638-A2.		
XX	29-JUN-2000.		
XX	02-DEC-1999;	99WO-US28565.	
XX	22-DEC-1998;	98US-0113296.	
XX	08-MAR-1999;	99WO-US05038.	
XX	21-APR-1999;	99US-0130232.	

Query Match	Best Local Similarity	100.0%; Score 1578; DB 21; Length 283;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 1	MEPPGDWPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDVPVSGCCPKSPG 60	
DB 1	MEPPGDWPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDVPVSGCCPKSPG 60	
QY 61	YRVVACGELTGTCTCEPCPPCTGTIAHLNGLSKCLQCQCDPAMGLRASRNCSTENAVCG 120	
DB 61	YRVVACGELTGTCTCEPCPPCTGTIAHLNGLSKCLQCQCDPAMGLRASRNCSTENAVCG 120	
QY 121	CSPGHFCTVODGDHCACRAVATSSPGORVQKGTESODTLQCNCPGTSPNLTLECCQ 180	
DB 121	CSPGHFCTVODGDHCACRAVATSSPGORVQKGTESODTLQCNCPGTSPNLTLECCQ 180	
QY 181	HQTKCSMLVTAKAGAGTSSSHVWVWFLEGSGLIVIVCSIVGLIICVKRRKPPGADVVKIVS 240	
DB 181	HQTKCSMLVTAKAGAGTSSSHVWVWFLEGSGLIVIVCSIVGLIICVKRRKPPGADVVKIVS 240	
QY 241	VQRKQBAEGEATVIEALQAPPDVTVVAVEETIPSPFGRSFNH 283	
DB 241	VQRKQBAEGEATVIEALQAPPDVTVVAVEETIPSPFGRSFNH 283	

RESULT 7
AAE20852
ID AAE20852 standard; Protein; 283 AA.
XX AAE20852;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human tumour necrosis factor receptor (TNFR) related protein.

CC treatment of arthritis or inflammation using an antibody directed against
 CC a fragment of the TR2 protein. TR2 its agonists, antagonists and
 CC antibodies exhibit cytostatic, dermatological, antianemic,
 CC immunosuppressive, antiallergic, antiarthritic, antiaesthetic,
 CC antiinflammatory, neuroprotective, nootropic, antiparkinsonian, and
 CC cerebroprotective activity. The methods are useful for treating arthritis
 CC or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
 CC mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an
 CC immunodeficiency or for enhancing an in vivo leukocyte response to an
 CC antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
 CC preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
 CC dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
 CC inflammatory myopathies) and immunodeficiency disorders (such as severely
 CC combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
 CC disorder, or Nezelof syndrome-combined immunodeficiency with IgA). TR2,
 CC TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
 CC antagonists are useful for treating or preventing autoimmune diseases and
 CC inhibit the growth, progression and/or metastasis of cancers. They are
 CC also used to activate, differentiate or proliferate cancerous cells or
 CC tissues, and can be used to treat diseases associated with increased cell
 CC survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
 CC Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful
 CC as sources for generating antibodies, as molecular weight markers.
 CC This sequence represents the TR2 receptor protein of the invention.

XX Sequence 283 AA;

Query Match 100.0%; Score 1578; DB 21; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1.3e-120;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPPRRSTPRTDVLRVLVLTFLGAPCAVAPALPSCKEDEYVPGSCCPKCSFG 60
 DB 1 MEPPGDMGPPPPRRSTPRTDVLRVLVLTFLGAPCAVAPALPSCKEDEYVPGSCCPKCSFG 60
 QY 61 YVKEACGELTGTVCPCPPGTYYIAHLNGLSKLCOCQCDPMGLRASNCRTEANAVCG 120
 DB 61 YVKEACGELTGTVCPCPPGTYYIAHLNGLSKLCOCQCDPMGLRASNCRTEANAVCG 120
 QY 121 CSPGHFCIVQDGDHCAACRAVATSSFGQVQKGTESQDTLCCNCPGTFSPNGTLEBCQ 180
 DB 121 CSPGHFCIVQDGDHCAACRAVATSSFGQVQKGTESQDTLCCNCPGTFSPNGTLEBCQ 180
 QY 181 HQTGCSMLVTKAGAGTSSSHWMMFLSGSLVIVIVYSTGILICVRRKRRPDGVKIVIVS 240
 DB 181 HQTGCSMLVTKAGAGTSSSHWMMFLSGSLVIVIVYSTGILICVRRKRRPDGVKIVIVS 240
 QY 241 VQRKQEGEATVIEALCAPPDVTVAVEETIPSTGRSPNH 283
 DB 241 VQRKQEGEATVIEALCAPPDVTVAVEETIPSTGRSPNH 283

RESULT 5

AA93695
 ID AA93695 standard; protein; 283 AA.

AC AA93695;

DT 03-OCT-2000 (first entry)

DE Amino acid sequence of novel polypeptide PRO509.

XX PRO201; PRO292; PRO327; PRO1265; PRO344; PRO347; PRO357;
 KW PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
 tumorigenesis; cancer; neoplastic cell growth; cell proliferation.

OS Homo sapiens.

XX Key location/Qualifiers

FT Peptide 1..36

FT Modified-site /note= "signal sequence"

FT /note= "N-myristoylation site"

FT Modified-site 89..95
 FT /note= "N-myristoylation site"
 FT Modified-site 104..110
 FT /note= "N-myristoylation site"
 FT Modified-site 110..114
 FT /note= "N-glycosylation site"
 FT Modified-site 120..126
 FT /note= "N-myristoylation site"
 FT Modified-site 153..159
 FT /note= "N-myristoylation site"
 FT Modified-site 173..177
 FT /note= "N-myristoylation site"
 FT Modified-site 193..199
 FT /note= "N-glycosylation site"
 FT Modified-site 195..201
 FT /note= "N-myristoylation site"
 FT Domain /note= "N-myristoylation site"
 FT /note= "transmembrane domain"
 FT Modified-site 220..226
 FT /note= "N-myristoylation site"
 FT Region 231..234
 FT /note= "cell attachment sequence"

XX WO200037640-A2.

XX 29-JUN-2000.

XX 16-DEC-1999; 99WO-US30095.

XX 22-DEC-1998; 98US-0113296.

XX 08-MAR-1999; 99WO-US05028.

XX 02-JUN-1999; 99WO-US12252.

XX 01-SEP-1998; 99WO-US20111.

XX 15-SEP-1998; 99WO-US21090.

XX 30-NOV-1999; 99WO-US28313.

XX 30-NOV-1999; 99WO-US28409.

XX 01-DEC-1999; 99WO-US28301.

XX 02-DEC-1999; 99WO-US28565.

XX (GENTH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
 PI Wood WJ;
 DR WPI: 2000-452188/39.
 DR N-PSDB; AAA46931.

XX New anti-polypeptide antibody useful in the treatment and diagnosis of
 PT neoplastic cell growth and proliferation -
 PS Claim 61; Fig 24; 220pp; English.

CC The present sequence represents a novel human polypeptide. The
 CC specification describes novel polypeptides designated PRO201, PRO292,
 CC PRO327, PRO1265, PRO343, PRO347, PRO357, PRO715, PRO1017,
 CC PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in
 CC the genome of tumour cells. The polypeptides are believed to contribute
 CC to tumorigenesis. The polypeptides are useful target for the
 CC identification of certain cancers, and may act as predictors of the
 CC prognosis of tumour treatment. Antibodies against these polypeptides
 CC are useful in the treatment and diagnosis of neoplastic cell growth
 CC and proliferation in mammals.

XX Sequence 283 AA;

XX Query Match 100.0%; Score 1578; DB 21; Length 283;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-120;
 XX Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPPRRSTPRTDVLRVLVLTFLGAPCAVAPALPSCKEDEYVPGSCCPKCSFG 60
 DB 1 MEPPGDMGPPPPRRSTPRTDVLRVLVLTFLGAPCAVAPALPSCKEDEYVPGSCCPKCSFG 60


```

RESULT 3
AA06488
ID AA06488 standard; Protein; 283 AA.
XX
XX AA06488;
XX
XX
XX
XX 27-SEP-1999 (first entry)
XX
XX Human tumour-associated protein PRO509.
XX
XX PRO1112; UNQ555; cancer; tumour necrosis factor receptor;
XX diagnosis; therapy; human.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FH Domain 201..225
XX FT /note="transmembrane domain"
XX FT 226..283
XX FT /note="cytoplasmic domain"
XX
XX
XX WO9935170-A2.
XX
XX 15-JUL-1999.
XX
XX
XX 05-JAN-1999; 99WO-US00106.
XX
XX
XX 20-NOV-1998; 98US-0109304.
XX PR 05-JAN-1998; 98US-0070440.
XX PR 29-APR-1998; 98US-0083500.
XX PR 22-MAY-1998; 98US-0086414.
XX PR 10-JUN-1998; 98US-0086742.
XX PR 10-NOV-1998; 98US-0107783.
XX
XX (GETH ) GENENTECH INC.
XX
XX Boetstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
XX Roy MA, Wood WT;
XX
XX WPI; 1999-430385/36.
XX DR N-PSDB; AAX87265.
XX
XX
XX Antibody against proteins expressed in neoplastic cells, useful for
XX tumor diagnosis and treatment
XX
XX
XX Example 1; Fig 24; 162pp; English.
XX
XX
XX This sequence represents human PRO509 (UNQ329), a protein encoded
XX by the novel cDNA clone DN50148 (see AAX87264), and a member of the
XX tumour necrosis factor receptor family. Amplification of DN50148
XX was observed in various tumour tissues, suggesting a role in tumour
XX formation or growth. Antagonists (e.g. antibodies) directed to
XX PRO509 may have use in cancer therapy. The invention identifies
XX 14 genes (see AAX87254-67) that are amplified in the genome of tumour
XX cells. Such amplification is expected to be associated with
XX overexpression of the gene product and to contribute to tumorigenesis.
XX The encoded proteins (see AA06477-90) may be useful targets for the
XX diagnosis and/or treatment (including prevention) of certain cancers,
XX and may act as predictors of the prognosis of tumour treatment.
XX Antibodies that bind the proteins are claimed and used in claimed
XX cancer diagnostic kits.
XX
XX
XX Sequence 283 AA;
XX
XX
XX Query Match 100.0%; Score 1578; DB 20; Length 283;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-120;
XX Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MPPGDMDGPPPPRRSRPTDTDVLRVLVYLFGLAPCYAPALPSCXDEYVGSCECPKCSPG 60
XX 1 MPPPDMDGPPPPRRSRPTDTDVLRVLVYLFGLAPCYAPALPSCXDEYVGSCECPKCSPG 60

```

QY	61	YKVKACCELTGTVCEPCPGTYIAHLNGLSKCLCQOMCDPAMGLRASNCSTENA	120
Db	61	YKVKACCELTGTVCEPCPGTYIAHLNGLSKCLCQOMCDPAMGLRASNCSTENA	120
QY	121	CSPGHFCIVODGDHCAACRAVATSSPGQRVQKGTESODTLQONCPGTFSPNGTLEECQ	180
Db	121	CSPGHFCIVODGDHCAACRAVATSSPGQRVQKGTESODTLQONCPGTFSPNGTLEECQ	180
QY	161	HOTKCSMLVTKAGAGTSSSHVWMLSGSLVIVICSTYGLIICVKRRKPRGDVVKVIYS	240
Db	161	HOTKCSMLVTKAGAGTSSSHVWMLSGSLVIVICSTYGLIICVKRRKPRGDVVKVIYS	240
QY	241	VQRKQBAEGEATVIEALQAPPDVTVAVEETIPSFTRGSPNH	263
Db	241	VQRKQBAEGEATVIEALQAPPDVTVAVEETIPSFTRGSPNH	263
RESULT 4			
AAV94721			
ID	AAV94721 standard; Protein; 263 AA.		
XX	AAV94721;		
XX	29-JAN-2001 (first entry)		
DE	Human TR2-receptor protein sequence.		
XX	Tumour necrosis factor-receptor related protein; TR2; human; cancer;		
KW	chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;		
KW	immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;		
KW	severely combined immunodeficiency; apoptosis inhibition;		
KW	Alzheimer's disease; Parkinson's disease; Crohn's disease.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	Key		
FH	Location/Qualifiers		
FT	Peptide 1..38		
FT	/note= "Signal peptide"		
FT	Protein 39..263		
FT	/label= "TR2 receptor"		
XX	MO200056405-A2.		
XX	28-SEP-2000.		
XX	22-MAR-2000; 2000WO-US07521.		
XX	22-MAR-1999; 99US-01256683.		
PR	26-MAR-1999; 99US-0126522.		
PR	20-MAY-1999; 99US-0135169.		
PR	06-AUG-1999; 99US-0147383.		
XX	(NIIJJ/) NI J.		
PA	(ROSE/) ROSEN C A.		
PA	(GENTZ/) GENTZ R L.		
PI	Ni J, Rosen CA, Gentz RL;		
XX	MPI, 2000-594519/56.		
DR	N-PSDB; AAA28149.		
XX	Nucleic acid molecule encoding a human tumor necrosis factor receptor 2		
PT	and its two splice variants, useful for treating arthritis or		
PT	inflammation, cancer (such as follicular lymphomas) and		
PT	immunodeficiency disorders -		
XX	Disclosure, Page 370; 373pp; English.		
ES	This invention relates to an isolated nucleic acid molecule encoding a		
CC	human tumor necrosis factor (TNF)-receptor related protein TR2. Included		
CC	in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.		
CC	The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a		
CC	member of the TNFR superfamily. The invention includes a method for the		

PF 27-APR-1995; 95WO-US05058.
 XX
 XX 27-APR-1995; 95WO-US05058.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Gentz R, NJ J, Rosen CA;
 XX
 XX WPI, 1996-497627/49.
 DR N-PSDB; AAT40048.
 XX
 XX New nucleic acid encoding a human tumour necrosis factor receptor -
 PT useful for treatment of auto-immune diseases etc., in diagnosis and
 PT for drug screening
 XX
 PS Claim 1; Pages 47-48, 73pp; English.
 XX
 XX The present sequence is the human tumour necrosis factor (TNF)
 CC receptor, which may be used for the identification of TNF receptor
 CC agonists or antagonists. TNF receptor agonists inhibit tumour
 CC growth, stimulate cell (e.g. T cell) differentiation, mediate the
 CC immune and antiviral responses, regulate growth, protect against
 CC radiation and Chlamydia infection, and can be used to treat
 CC immunodeficiencies, e.g. human immunodeficiency virus. Antagonists
 CC can be used to treat T cell mediated autoimmune disease,
 CC inflammation, septic shock, cerebral malaria, cachexia or B cell
 CC cancers, to inhibit graft-host reactions and to prevent apoptosis
 CC or cytotoxicity. Fragments of the TNF receptor encoding DNA can be
 CC used as hybridisation probes for detecting related genes.
 CC Antibodies against the protein can be used as reagents for
 CC detecting/measuring soluble forms of protein in the circulation.
 XX

Sequence 283 AA;

Query Match 100.0%; Score 1578; DB 17; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1.3e-120;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPMRSTRPTDVLRLVLTFLGAPCAPALPSCKEDEYPVGSCECPKCSFG 60
 DB 1 MEPPGDMGPPPMRSTRPTDVLRLVLTFLGAPCAPALPSCKEDEYPVGSCECPKCSFG 60
 QY 61 YRKEACGELTGVCPCPGTYIAHLNGLSKLCOCMDPMGLRASNCRTENAACG 120
 DB 61 YRKEACGELTGVCPCPGTYIAHLNGLSKLCOCMDPMGLRASNCRTENAACG 120
 QY 121 CSPGHFCIVQDDGHCACRAVATSSPGQRYQKGTESODTLQNCPCPGTFSPNGTLEECQ 180
 DB 121 CSPGHFCIVQDDGHCACRAVATSSPGQRYQKGTESODTLQNCPCPGTFSPNGTLEECQ 180
 QY 181 HQTKCSWLVTYKAGAGTSSSHWMMFLSGSLVIVICSTYGLIICVRRKPRGDVVKIVS 240
 DB 181 HQTKCSWLVTYKAGAGTSSSHWMMFLSGSLVIVICSTYGLIICVRRKPRGDVVKIVS 240
 QY 241 VQRKQEAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283
 DB 241 VQRKQEAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283

RESULT 2
 AAM69238
 ID AAM69238 standard; Protein; 283 AA.

AC AAM69238;
 XX
 XX 21-OCT-1998 (first entry)
 XX
 DE Herpesvirus entry mediator protein.
 XX
 KW Entry mediator gene; herpesvirus; HVEM; tumour necrosis factor receptor;
 KW gene expression regulator; cellular stress; inflammatory response;
 KW lymphocyte activity regulator; autoimmune response.
 XX

OS Homo sapiens.
 XX
 XX WO9825967-A1.
 XX
 XX 18-JUN-1998.
 PD
 XX
 XX 05-DEC-1997; 97WO-US222278.
 PF
 XX
 XX 12-DEC-1996; 96US-0032705.
 PR
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX
 XX Ashkenazi AJ, Marsters SA;
 PI
 XX
 XX WPI, 1998-348457/30.
 DR N-PSDB; AAV44852.
 DR
 XX
 XX Herpesvirus entry mediator polypeptide, HVEM - useful, e.g. in
 PT assays for HVEM and to produce antibodies and transgenic animals,
 PT e.g. for drug screening
 XX
 PS Claim 1; Fig 1; 46pp; English.

CC This sequence is the herpesvirus entry mediator (HVEM) protein of
 CC the invention. The protein is useful in quantitative diagnostic assays
 CC for HVEM, in affinity purification of HVEM from recombinant cells/natural
 CC sources and in competitive-type receptor binding assays. It can also be
 CC used to generate antibodies, also useful in diagnostic assays for HVEM
 CC and affinity purification of HVEM. HVEM is believed to be a member of the
 CC tumour necrosis factor receptor (TNFR) family, and transient transfection
 CC of HVEM into human 293 cells caused marked activation of certain
 CC transcription factors, e.g. AP-1, suggesting that HVEM is involved in
 CC regulating gene expression in response to infectious stimuli and cellular
 CC stresses. The predominant expression of HVEM mRNA in lymphocyte-rich
 CC tissues (e.g. spleen and peripheral blood) also suggested it may be a
 CC receptor in regulating lymphocyte activity. Antibodies produced may
 CC therefore be useful therapeutically, e.g. antagonistic antibodies may be
 CC useful to block excessive inflammatory/autoimmune response resulting from
 CC e.g. AP-1 induction, whilst agonistic antibodies may enhance HVEM
 CC regulation of such induction. The DNA may be used diagnostically, e.g.
 CC to determine if DNA and/or RNA encoding HVEM is present in cells, and to
 CC to prepare HVEM polypeptide recombinantly. It is also useful to produce
 CC non-human transgenic animals (e.g. mice or rats), especially knockout
 CC animals containing cells with an altered gene encoding HVEM polypeptide.
 CC Such animals are useful in the development and screening of
 CC therapeutically useful reagents.

Sequence 283 AA;

Query Match 100.0%; Score 1578; DB 19; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1.3e-120;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPDGMGPPPMRSTRPTDVLRLVLTFLGAPCAPALPSCKEDEYPVGSCECPKCSFG 60
 DB 1 MEPPDGMGPPPMRSTRPTDVLRLVLTFLGAPCAPALPSCKEDEYPVGSCECPKCSFG 60
 QY 61 YRKEACGELTGVCPCPGTYIAHLNGLSKLCOCMDPMGLRASNCRTENAACG 120
 DB 61 YRKEACGELTGVCPCPGTYIAHLNGLSKLCOCMDPMGLRASNCRTENAACG 120
 QY 121 CSPGHFCIVQDDGHCACRAVATSSPGQRYQKGTESODTLQNCPCPGTFSPNGTLEECQ 180
 DB 121 CSPGHFCIVQDDGHCACRAVATSSPGQRYQKGTESODTLQNCPCPGTFSPNGTLEECQ 180
 QY 181 HQTKCSWLVTYKAGAGTSSSHWMMFLSGSLVIVICSTYGLIICVRRKPRGDVVKIVS 240
 DB 181 HQTKCSWLVTYKAGAGTSSSHWMMFLSGSLVIVICSTYGLIICVRRKPRGDVVKIVS 240
 QY 241 VQRKQEAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283
 DB 241 VQRKQEAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283

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OM protein - protein search, using sw model

Run on: November 14, 2003, 17:26:45 ; Search time 40 Seconds

(without alignments)
1122.991 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 1578

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*

3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*

4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*

5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*

6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*

7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*

8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*

9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*

10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*

11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*

12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*

13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*

14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*

15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*

16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*

17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*

18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*

19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*

20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*

21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*

22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1578	100.0	283	AAW05809	Human tumour necro
2	1578	100.0	283	AAW69238	Herpesvirus entry
3	1578	100.0	283	AAW06488	Human tumour-assoc
4	1578	100.0	283	AAW94721	Human TR2-receptor
5	1578	100.0	283	AAW93695	Amino acid sequenc
6	1578	100.0	283	AAW95348	Human PRO509 antic
7	1578	100.0	283	AAW20852	Human tumour necro
8	1578	100.0	283	ABR40215	Human cohesin. Ho
9	1578	100.0	283	ABU60681	Human membrane-bou

10	1575	99.8	283	AAW60045	Human TNF receptor
11	1575	99.8	283	AAW87591	Human tumour necro
12	1575	99.8	283	AAW94717	Human TR2-receptor
13	1572	99.6	283	AAW65031	Tumour necrosis fa
14	1570	99.5	283	AAW12659	Human herpes simpl
15	1570	99.5	283	AAW05797	Herpes virus entry
16	1373.5	87.0	277	AAW79207	Membrane-bound her
17	1373.5	87.0	277	AAW60694	Human membrane-bou
18	1152.5	73.0	239	ABU60695	Human mature membr
19	1068	67.7	193	AAW79204	Soluble herpesvtru
20	1068	67.7	193	ABU60675	Human soluble Herp
21	1060	67.2	197	AAW79205	Soluble herpesvtru
22	1060	67.2	197	ABU60682	Human soluble Herp
23	1058	67.0	186	AAW79206	Soluble herpesvtru
24	1058	67.0	186	ABU60688	Human soluble Herp
25	847	53.7	155	ABU60676	Human mature solub
26	843	53.4	148	ABU60689	Human mature solub
27	839	53.2	159	ABU60683	Human mature solub
28	604.5	38.3	185	AAW60046	Human TNF receptor
29	604.5	38.3	185	AAW94716	Human TR2-receptor
30	604.5	38.3	240	AAW05810	Human tumour necro
31	393	24.9	136	AAW60047	Human TNF receptor
32	393	24.9	136	AAW94719	Human TR2-receptor
33	377.5	23.9	134	AAW05811	Human tumour necro
34	332	21.0	278	AAW95322	Pig costimulatory
35	276.5	17.5	281	AAW94715	Murine CD40 protei
36	268.5	17.0	277	AAW32191	CD40 protein. Uni
37	267.5	17.0	276	AAW33499	Human CD40 protein
38	267.5	17.0	277	AAW38859	CD40 protein. Hom
39	267.5	17.0	277	AAW52701	Human CD40 protein
40	267.5	17.0	277	AAW84892	Human CD40 antigen
41	267.5	17.0	277	AAW50520	Human tumour necro
42	267.5	17.0	277	AAW37807	Human CD40. Homo
43	267.5	17.0	277	AAW018051	CD40 B-cell antige
44	267.5	17.0	277	AAW19354	Human CD40 antigen
45	267.5	17.0	277	ABR40010	Human Moxifin. Ho

ALIGNMENTS

RESULT 1	
AAW05809	AAW05809 standard; Protein; 283 AA.
ID	AAW05809;
XX	30-JUN-1997 (first entry)
XX	Human tumour necrosis factor receptor.
XX	Human, tumour necrosis factor; TNF; receptor; treatment;
XX	activation; inhibition; identification; agonist; antagonist;
XX	stimulation; T cell; differentiation; mediation; immune;
XX	antiviral; response; regulation; growth; protection; HIV;
XX	radiation; Chlamydia; infection; immunodeficiency; virus;
XX	autoimmune disease; inflammation; septic shock; cerebral;
XX	cachexia; B cell; cancer; graft; host; reaction; rejection;
XX	prevention; apoptosis; cytotoxicity; hybridisation probe;
XX	detection; antibody; reagent.
XX	Homo sapiens.
XX	Key
XX	Peptide
XX	Location/Qualifiers
XX	1..38
XX	/label= sig_peptide
XX	39..283
XX	/label= mat_peptide
XX	WO9634095-A1.
XX	31-OCT-1996.

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-041-886-27

Query Match 17.0%; Score 267.5; DB 3; Length 276;
Best Local Similarity 26.1%; Pred. No. 2,1e-16;
Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;

QY 20 VRLVLYLFLGAPCYAPAL-----PSCKEDEVPGSECCPKCSPGYRVKACGELTGV 74
DB 1 MVRLLPQCVMWG--CLLTAVHPEPPTACREKQYLINSQCCSLQCPQKLVSDCTEFTETE 58
QY 75 CERCPRGTYIAHNGSKLQCCMDPANGLRASRNCSTENAVGCGSPGHFCIVQDDGH 134
DB 59 CLPCGSEFPLDTWNRETHCHQHKYCDPNLGLRVQKGTSETPTICTCEBGMHC--TSEA 115
QY 135 CAACRAVATSSPGQAVQKGTESQDTLCONCPPTFS--PNGTLEBQHOTKCSW--LVTK 191
DB 116 CESCVAHRSCSPGFGVKQATGSDTICBPCPVGFSNVSAFEKCHPWTSCETKDLVQ 175
QY 192 AAGTSSSHVWVWFSLVIVICSTVGLICVKKRRKRGDVVKVIVSVQRRQDAEGE 251
DB 176 Q-AGTKTIDVCGPQDRALALVPIPIFGILFA-----ILLVIVFIKKVAKKPTNK 225
QY 252 ATVIELQAPPDV-----TTAVBETI 273
DB 226 AP--HPKQEPQETINPPDDLPGSNTAAPVOETL 255

Search completed: November 14, 2003, 17:32:51
Job time : 22 secs

US-09-146-950-20
; Sequence 20, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-146-950-20

Query Match 53.2%; Score 839; DB 3; Length 159;
Best Local Similarity 98.0%; Pred. No. 4,8e-68;
Matches 146; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 39 LPSCKEDEYVPGSECCPKSPGYRKEACGELTGTVCPCPPGTYYIAHLNGLSKLQCOM 98
DB 1 LPSCKEDEYVPGSECCPKSPGYRKEACGELTGTVCPCPPGTYYIAHLNGLSKLQCOM 60
QY 99 CDPAMGLRASRNCSTENAVCGSPGHFCIVODGDHCAACRAVATSSPGORVOKGSGTESQ 158
DB 61 CDPAMGLRASRNCSTENAVCGSPGHFCIVODGDHCAACRAVATSSPGORVOKGSGTESQ 120
QY 159 DTLQNCPPGTGTFSPNGTLEBQCHOTKCSW 187
DB 121 DTLQNCPPGTGTFSPNGTLEBQCHOTKCSW 147

RESULT 13
US-09-146-950-25
; Sequence 25, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-146-950-25

Query Match 23.1%; Score 365; DB 3; Length 77;
Best Local Similarity 95.5%; Pred. No. 7,7e-26;
Matches 64; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 121 CSPGHFCIVODGDHCAACRAVATSSPGORVOKGSGTESQDTLQNCPPGTGTFSPNGTLEBQ 180
DB 1 CSPGHFCIVODGDHCAACRAVATSSPGORVOKGSGTESQDTLQNCPPGTGTFSPNGTLEBQ 60
QY 181 HOTKCSW 187
DB 61 HOT--NW 65

RESULT 14
US-09-042-785A-11
; Sequence 11, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J

TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-042-785A-11

Query Match 17.5%; Score 276.5; DB 3; Length 289;
Best Local Similarity 27.9%; Pred. No. 3,4e-17;
Matches 69; Conservative 43; Mismatches 106; Indels 29; Gaps 8;

QY 41 SCKEDYVPGSECCPKSPGYRKEACGELTGTVCPCPPGTYYIAHLNGLSKLQCOMCD 100
DB 25 TCSDKQYVHGGCCDLCQPSRLSHHTALEKTQCHPCDSGERSAQNRRIRCHQHNC 84
QY 101 PAMGLRASRNCSTENAVCGSPGHFCIVODGDHCAACRAVATSSPGORVOKGSGTESQDT 160
DB 85 PNOGLRYKKEGTAEPTVCTCKEGCHTCKD--CEACAQHTPCIPGFGVEMATETTD 141
QY 161 LQNCPPGTGTFSPNGTLEBQCHOTKCS---WLVTKAGNTSSSHWVWFLSGSLVIV 215
DB 142 VCHPCPVGFPSNOSLFEKCYPTWSCBDKNLEVLQK--GTSOTNYICGLKSMRALVI 198
QY 216 CSTVGLIIC-----VKR--RKPRGDVVKIVSVORKEAGEATVIEALQAPDVT 266
DB 199 PVVMGLITITFGVFLVKKVKKXPN--EMLPABARQDPQWME-----DYPGHNTA 249
QY 267 VAVEBTI 273
DB 250 APVQETL 256

RESULT 15
US-09-041-886-27
; Sequence 27, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabinzaden, Sharrow
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:

NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-09-631-780-7

Query Match
Best Local Similarity 100.0%; Score 1073; DB 4; Length 419;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDEYVGSSECCPKCSFG 60
DB 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDEYVGSSECCPKCSFG 60
QY 61 YVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPMGLRASRNCSTENAVCG 120
DB 61 YVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESODTLCONCPGTFSPNGTLEBQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESODTLCONCPGTFSPNGTLEBQ 180
QY 181 HOTKC 185
DB 181 HOTKC 185

RESULT 9
US-09-146-950-2
Sequence 2, Application US/09146950A
Patent No. 6287808

GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-2

Query Match
Best Local Similarity 98.4%; Score 1068; DB 3; Length 193;
Matches 184; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDEYVGSSECCPKCSFG 60
DB 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDEYVGSSECCPKCSFG 60
QY 61 YVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPMGLRASRNCSTENAVCG 120
DB 61 YVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESODTLCONCPGTFSPNGTLEBQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESODTLCONCPGTFSPNGTLEBQ 180
QY 181 HOTKC 187
DB 181 HOTKC 187

RESULT 10
US-09-146-950-18
Sequence 18, Application US/09146950A
Patent No. 6287808

GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 197
TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-18

Query Match
Best Local Similarity 98.4%; Score 1060; DB 3; Length 197;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDEYVGSSECCPKCSFG 60
DB 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDEYVGSSECCPKCSFG 60
QY 61 YVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPMGLRASRNCSTENAVCG 120
DB 61 YVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESODTLCONCPGTFSPNGTLEBQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESODTLCONCPGTFSPNGTLEBQ 180
QY 181 HOTKC 187
DB 181 HOTKC 187

RESULT 11
US-09-146-950-4
Sequence 4, Application US/09146950A
Patent No. 6287808

GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 155
TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-4

Query Match
Best Local Similarity 98.0%; Score 847; DB 3; Length 155;
Matches 146; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 39 LPSCKEDEYVGSSECCPKCSFGYVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCM 98
DB 1 LPSCKEDEYVGSSECCPKCSFGYVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCM 98
QY 99 CDPAMGLRASRNCSTENAVCGCSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESQ 158
DB 99 CDPAMGLRASRNCSTENAVCGCSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESQ 158
QY 159 DTLCONCPGTFSPNGTLEBQHOTKC 187
DB 159 DTLCONCPGTFSPNGTLEBQHOTKC 187

RESULT 12

APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/333,279
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-333-279-2

Query Match 100.0%; Score 1578; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.8e-134;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMWRSTRTDVLRLVLYLFLGAPCYAPALPSCKEDEYVPGSECCPKCSFG 60
DB 1 MEPPGDMGPPMWRSTRTDVLRLVLYLFLGAPCYAPALPSCKEDEYVPGSECCPKCSFG 60
QY 61 YRKEACGELTGVCPCPGTYIAHLNGLSKLCCOMCDPAMGLASRNCSTENAVCG 120
DB 61 YRKEACGELTGVCPCPGTYIAHLNGLSKLCCOMCDPAMGLASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLCCNCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLCCNCPGTFSPNGTLEECQ 180
QY 181 HOTKCSWLVTYKAGATSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVAVIYS 240
DB 181 HOTKCSWLVTYKAGATSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVAVIYS 240
QY 241 VORRQEAEGEATVIEALQAPPDVTTVAEETIPSTGSPNH 283
DB 241 VORRQEAEGEATVIEALQAPPDVTTVAEETIPSTGSPNH 283

RESULT 3
US-09-631-780-2
Sequence 2, Application US/09631780
Patent No. 6573058
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/631,780
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US/08/509,024B
PRIOR FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-631-780-2

Query Match 100.0%; Score 1578; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.8e-134;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMWRSTRTDVLRLVLYLFLGAPCYAPALPSCKEDEYVPGSECCPKCSFG 60
DB 1 MEPPGDMGPPMWRSTRTDVLRLVLYLFLGAPCYAPALPSCKEDEYVPGSECCPKCSFG 60
QY 61 YRKEACGELTGVCPCPGTYIAHLNGLSKLCCOMCDPAMGLASRNCSTENAVCG 120
DB 61 YRKEACGELTGVCPCPGTYIAHLNGLSKLCCOMCDPAMGLASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLCCNCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLCCNCPGTFSPNGTLEECQ 180

DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLCCNCPGTFSPNGTLEECQ 180
QY 181 HOTKCSWLVTYKAGATSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVAVIYS 240
DB 181 HOTKCSWLVTYKAGATSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVAVIYS 240
QY 241 VORRQEAEGEATVIEALQAPPDVTTVAEETIPSTGSPNH 283
DB 241 VORRQEAEGEATVIEALQAPPDVTTVAEETIPSTGSPNH 283

RESULT 4
US-09-072-993C-2
Sequence 2, Application US/09072993C
Patent No. 6346388
GENERAL INFORMATION:
APPLICANT: Michael R. Brigham-Burke
APPLICANT: Peter R. Young
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
FILE REFERENCE: GH-50030
CURRENT APPLICATION NUMBER: US/09/072,993C
CURRENT FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/055,513
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 60/056,980
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/057,550
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-072-993C-2

Query Match 99.6%; Score 1572; DB 4; Length 283;
Best Local Similarity 99.6%; Pred. No. 1.3e-133;
Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMWRSTRTDVLRLVLYLFLGAPCYAPALPSCKEDEYVPGSECCPKCSFG 60
DB 1 MEPPGDMGPPMWRSTRTDVLRLVLYLFLGAPCYAPALPSCKEDEYVPGSECCPKCSFG 60
QY 61 YRKEACGELTGVCPCPGTYIAHLNGLSKLCCOMCDPAMGLASRNCSTENAVCG 120
DB 61 YRKEACGELTGVCPCPGTYIAHLNGLSKLCCOMCDPAMGLASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLCCNCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLCCNCPGTFSPNGTLEECQ 180
QY 181 HOTKCSWLVTYKAGATSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVAVIYS 240
DB 181 HOTKCSWLVTYKAGATSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVAVIYS 240
QY 241 VORRQEAEGEATVIEALQAPPDVTTVAEETIPSTGSPNH 283
DB 241 VORRQEAEGEATVIEALQAPPDVTTVAEETIPSTGSPNH 283

RESULT 5
PCT-US96-12374-2
Sequence 2, Application PC/TUS9612374
GENERAL INFORMATION:
APPLICANT: Northwestern University
TITLE OF INVENTION: Herpes Virus Entry Mediator
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSER: Dressler, Goldsmith, Milmanow & Katz, Ltd.
STREET: 180 N. Stetson, Suite 4700
CITY: Chicago

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2003, 17:29:30 ; Search time 21 Seconds
(without alignments)
570.189 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 1578
Sequence: 1 MEPPGDMGPPWRSTPRTDV.....VTVAVEETIPSTGRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1578	100.0	283	3	US-08-509-024-2
2	1578	100.0	283	4	US-09-333-279-2
3	1578	100.0	283	4	US-09-631-780-2
4	1572	99.6	283	4	US-09-072-993C-2
5	1570	99.5	283	5	PCT-US96-12374-2
6	1073	68.0	419	3	US-08-509-024-7
7	1073	68.0	419	4	US-09-333-279-7
8	1073	68.0	419	4	US-09-631-780-7
9	1068	67.7	193	4	US-09-146-950-2
10	1060	67.2	197	3	US-09-146-950-18
11	847	53.7	155	3	US-09-146-950-4
12	839	53.2	159	3	US-09-146-950-20
13	365	23.1	77	3	US-09-146-950-25
14	276.5	17.5	289	3	US-09-042-785A-11
15	267.5	17.0	276	3	US-09-041-886-27
16	267.5	17.0	277	3	US-09-042-785A-10
17	267.5	17.0	277	3	US-09-006-353A-10
18	267.5	17.0	277	4	US-08-114-944D-2
19	267.5	17.0	277	4	US-09-573-986-10
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21	260	16.5	207	3	US-08-974-022-47
22	260	16.5	207	3	US-08-795-445A-47
23	260	16.5	207	3	US-08-795-447A-47
24	260	16.5	207	3	US-08-974-186-47
25	260	16.5	207	3	US-08-795-446B-47
26	260	16.5	207	4	US-08-706-945D-133
27	260	16.5	325	1	US-08-292-549-2

28	260	16.5	325	3	US-09-042-785A-9	Sequence 9, Appli
29	260	16.5	325	5	PCT-US91-02207-2	Sequence 2, Appli
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31	259	16.4	227	3	US-08-974-022-48	Sequence 48, Appli
32	259	16.4	227	3	US-08-795-445A-48	Sequence 48, Appli
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37	259	16.4	235	4	US-09-326-194-4	Sequence 4, Appli
38	259	16.4	235	4	US-09-580-235-4	Sequence 4, Appli
39	259	16.4	235	4	US-09-580-235-8	Sequence 8, Appli
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41	259	16.4	235	4	US-09-580-181-8	Sequence 8, Appli
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43	259	16.4	235	4	US-09-102-530-8	Sequence 8, Appli
44	259	16.4	257	4	US-09-579-845-10	Sequence 10, Appli
45	259	16.4	461	1	US-08-385-229-2	Sequence 2, Appli

ALIGNMENTS

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US-08-509-024-2
; Sequence 2, Application US/08509024B
; Parent No. 6291207
; GENERAL INFORMATION:
; APPLICANT: SPEAR, Patricia G.
; TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
; FILE REFERENCE: 0290-1
; CURRENT APPLICATION NUMBER: US/08/509,024B
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-509-024-2

Query Match      100.0%; Score 1578; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 3; 8e-134; Indels 0; Gaps 0;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 CSPHFCITVDGDHCAACRAVATSSPGORVOKGTESDTLACNCPGTSPNGTLEECQ 180
QY 181 HQTKCSMLVTKAGAGTSSHWMMFLSGSLVIYIVCSVGLIICVKRRKRGDVVKYIVS 240
DB 181 HQTKCSMLVTKAGAGTSSHWMMFLSGSLVIYIVCSVGLIICVKRRKRGDVVKYIVS 240
QY 241 VORRQGEABEATVIEALQAPDVTYVAVEETIPSTGRSPNH 283
DB 241 VORRQGEABEATVIEALQAPDVTYVAVEETIPSTGRSPNH 283

RESULT 2
US-09-333-279-2
; Sequence 2, Application US/09333279
; Parent No. 630336
; GENERAL INFORMATION:
; APPLICANT: SPEAR, Patricia G.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 17:30:26 ; Search time 175 Seconds

(without alignments)
1471.469 Million cell updates/sec

Title: US-08-741-095B-26
Perfect score: 1578

Sequence: 1 MEPPGDMGPPWRKSTPRDV.....VTYVAVEETIPSTGRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match
Maximum Match

Listing first

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1578	100.0	283	1	PCT-US01-26396-31	Sequence 31, Appl

2	1578	100.0	283	1	PCT-US02-29560-288	Sequence 288, App
3	1578	100.0	283	1	PCT-US03-10956-48	Sequence 48, Appl
4	1578	100.0	283	1	PCT-US95-05058-2	Sequence 2, Appl
5	1578	100.0	283	1	PCT-US99-20180-13	Sequence 13, Appl
6	1578	100.0	283	8	US-08-462-315-2	Sequence 2, Appl
7	1578	100.0	283	8	US-08-462-315-2	Sequence 2, Appl
8	1578	100.0	283	8	US-08-462-315-2	Sequence 2, Appl
9	1578	100.0	283	11	US-08-741-095B-26	Sequence 26, Appl
10	1578	100.0	283	13	US-08-987-902-1	Sequence 13, Appl
11	1578	100.0	283	17	US-09-342-767-13	Sequence 1, Appl
12	1578	100.0	283	18	US-09-480-284-1	Sequence 1, Appl
13	1578	100.0	283	19	US-09-533-262-26	Sequence 26, Appl
14	1578	100.0	283	22	US-09-791-537-41397	Sequence 41397, A
15	1578	100.0	283	23	US-09-882-636-46	Sequence 46, Appl
16	1578	100.0	283	23	US-09-886-342-60	Sequence 60, Appl
17	1578	100.0	283	24	US-09-924-231-2	Sequence 2, Appl
18	1578	100.0	283	24	US-09-934-289A-13	Sequence 13, Appl
19	1578	100.0	283	24	US-09-935-727-31	Sequence 31, Appl
20	1578	100.0	283	28	US-10-245-882-288	Sequence 288, App
21	1578	100.0	283	29	US-10-369-300-2	Sequence 2, Appl
22	1578	100.0	283	30	US-10-410-308-42	Sequence 42, Appl
23	1578	100.0	283	30	US-10-418-242-31	Sequence 31, Appl
24	1578	100.0	283	32	US-10-418-242-31	Sequence 31, Appl

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rpm and .rpm

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapm

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

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RESULT 1
PCT-US01-26396-31
; Sequence 31, Application PC/TUS0126396
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: P454PC73
; CURRENT APPLICATION NUMBER: PCT/US01/26396
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US01-26396-31
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Matches 283; Conservative 0; Mismatches 0;

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QY 61 YRVKACGELTGTCCEPCPGTYIAHLNGLSKLCQCCDPAMGIRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTCCEPCPGTYIAHLNGLSKLCQCCDPAMGIRASRNCSTENAVCG 120
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DB 121 CSPGHFCTVQGDHCAACRAVATSSPGQVKGSTESODTLCCNCPPTFSFNGTLESCQ 180
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DB 181 HOTKCSMLVTAKAGTSSSHVWVWFLSGSLVIVICSTVGLICVKRRKPGDVVKVIVS 240
QY 241 VÖRRÖABEGEATVIEALQAPPDVTVVAEETIPSTGRSPNH 283
DB 241 VÖRRÖABEGEATVIEALQAPPDVTVVAEETIPSTGRSPNH 283

RESULT 2

PCT-US02-29560-288
; Sequence 288, Application PC/TUS0229560
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevez, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560
; PRIOR FILING DATE: 2025-11-01
; PRIOR APPLICATION NUMBER: US 60/323,469
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 288
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29560-288

Query Match 100.0%; Score 1578; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119; Indels 0; Gaps 0;
Matches 283; Conservative 0; Mismatches 0;

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DB 61 YRVKACGELTGTCCEPCPGTYIAHLNGLSKLCQCCDPAMGIRASRNCSTENAVCG 120
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DB 121 CSPGHFCTVQGDHCAACRAVATSSPGQVKGSTESODTLCCNCPPTFSFNGTLESCQ 180
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DB 181 HOTKCSMLVTAKAGTSSSHVWVWFLSGSLVIVICSTVGLICVKRRKPGDVVKVIVS 240
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DB 241 VÖRRÖABEGEATVIEALQAPPDVTVVAEETIPSTGRSPNH 283

DB 241 VÖRRÖABEGEATVIEALQAPPDVTVVAEETIPSTGRSPNH 283

RESULT 3

PCT-US03-10956-48
; Sequence 48, Application PC/TUS0310956
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Specifically Bind to T15
; FILE REFERENCE: PF581PCT
; CURRENT APPLICATION NUMBER: PCT/US03/10956
; PRIOR FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 60/372,087
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-10956-48

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Best Local Similarity 100.0%; Pred. No. 7.2e-119; Indels 0; Gaps 0;
Matches 283; Conservative 0; Mismatches 0;

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RESULT 4

PCT-US95-05058-2
; Sequence 2, Application PC/TUS9505058
; GENERAL INFORMATION:
; APPLICANT: NI, ET AL.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESS: CROCHT, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05058
; FILING DATE: Concurrently
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-255
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-05058-2

Query Match 100.0%; Score 1578; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 7,2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEPPGDMGPPMRSPTRTDVLRLVLYLFTLGPVAPALPSCKEDEYPVGSECCPKCSFG 60
QY 61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLQCCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLQCCMCDPAMGLRASRNCSTENAVCG 120
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DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQRVQKGTESQDTLQNCPPGTSPNGTLEECQ 180
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DB 181 HQTKCSMLVTKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKRGRGVVAVYIS 240
QY 241 VQRKQAEAGEATVIEALQAPDVTVAVETIIPSTGSRPNH 283
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RESULT 5
PCT-US99-20180-13
Sequence 13, Application PC/TUS9920180
GENERAL INFORMATION:
APPLICANT: Millennium Biotherapeutics, Inc.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: 09404/079M01
CURRENT APPLICATION NUMBER: PCT/US99/20180
EARLIER FILING DATE: 1999-09-03
EARLIER APPLICATION NUMBER: US 09/342,767
EARLIER FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6
US-08-462-315-2
Sequence 2, Application US/08462315
GENERAL INFORMATION:
APPLICANT: NI, ET AL.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: June 5, 1995
APPLICATION NUMBER: US/08/462,315
CLASSIFICATION: 514
Prior Application Data:
APPLICATION NUMBER: PCT/US95/05058
FILING DATE: 27 APR 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-462-315-2

Query Match 100.0%; Score 1578; DB 8; Length 283;
Best Local Similarity 100.0%; Pred. No. 7,2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMRSPTRTDVLRLVLYLFTLGPVAPALPSCKEDEYPVGSECCPKCSFG 60
DB 1 MEPPGDMGPPMRSPTRTDVLRLVLYLFTLGPVAPALPSCKEDEYPVGSECCPKCSFG 60
QY 61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLQCCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLQCCMCDPAMGLRASRNCSTENAVCG 120

QY 121 CSPGHFCIVODGDHCAACRAVATSSPGORVOKGTESDTLCONCPGTFSPNGTLEEQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGORVOKGTESDTLCONCPGTFSPNGTLEEQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
QY 241 VORKROEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
DB 241 VORKROEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 7
US-08-462-962-2
Sequence 2, Application US/08462962
GENERAL INFORMATION:
APPLICANT: NI, ET AL.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,962
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05058
FILING DATE: 27 APR 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-422
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-462-962-2

Query Match 100.0%; Score 1578; DB 8; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
QY 241 VORKROEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
DB 241 VORKROEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 8
US-08-464-595-2
Sequence 2, Application US/08464595
GENERAL INFORMATION:
APPLICANT: JIAN NI, REINER GENTZ AND CRAIG ROSEN
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,595
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05058
FILING DATE: April 27, 1995
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-464-595-2

Query Match 100.0%; Score 1578; DB 8; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 VORRQOAEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 9

US-08-741-095b-26
Sequence 26, Application US/08741095B
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig
APPLICANT: Genz, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-like 2
FILE REFERENCE: 1488.0770004
CURRENT APPLICATION NUMBER: US/08/741,095B
CURRENT FILING DATE: 1996-10-30
PRIOR APPLICATION NUMBER: US 08/464,595
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/462,962
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/462,315
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: PCT/US95/05058
PRIOR FILING DATE: 1995-04-27
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.0
SEQ ID NO 26
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-08-741-095b-26

Query Match 100.0%; Score 1578; DB 11; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDEYPVGSCECPKCSPG 60
Db 1 MEPPGDMGPPMRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDEYPVGSCECPKCSPG 60
QY 61 YRVKACGELTGTVECEPCPGTYIAHLNGLSKLQCOMCDPAMGLRASNCRSTENAVCG 120
Db 61 YRVKACGELTGTVECEPCPGTYIAHLNGLSKLQCOMCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCTVQDDHCAACRAVATSSPGQVQKGTESQDTLQONCPGTFSPNGTLEECQ 180
Db 121 CSPGHFCTVQDDHCAACRAVATSSPGQVQKGTESQDTLQONCPGTFSPNGTLEECQ 180
QY 181 HOTKSMVLTAKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
Db 181 HOTKSMVLTAKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
QY 241 VORRQOAEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
Db 241 VORRQOAEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 10

US-08-987-902-1
Sequence 1, Application US/08987902
GENERAL INFORMATION:
APPLICANT: Avi J. Aabkenazi and Scot A. Marssters
TITLE OF INVENTION: HYEM Polypeptides and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,902
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1068R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-987-902-1

Query Match 100.0%; Score 1578; DB 13; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDEYPVGSCECPKCSPG 60
Db 1 MEPPGDMGPPMRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDEYPVGSCECPKCSPG 60
QY 61 YRVKACGELTGTVECEPCPGTYIAHLNGLSKLQCOMCDPAMGLRASNCRSTENAVCG 120
Db 61 YRVKACGELTGTVECEPCPGTYIAHLNGLSKLQCOMCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCTVQDDHCAACRAVATSSPGQVQKGTESQDTLQONCPGTFSPNGTLEECQ 180
Db 121 CSPGHFCTVQDDHCAACRAVATSSPGQVQKGTESQDTLQONCPGTFSPNGTLEECQ 180
QY 181 HOTKSMVLTAKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
Db 181 HOTKSMVLTAKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
QY 241 VORRQOAEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
Db 241 VORRQOAEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 11

US-09-342-767-13
Sequence 13, Application US/09342767
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: M81098-061CPI
CURRENT APPLICATION NUMBER: US/09/342,767
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(38)
US-09-342-767-13

Query Match 100.0%; Score 1578; DB 17; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPGDGMPWRSPRTDVLRLVLYLFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
DB 1 MPPGDGMPWRSPRTDVLRLVLYLFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
QY 61 YRKEACGELTGTVCPCPGTYIAHLNLSKLCQCMCDPAMGLRASNCRSTENAVCG 120
DB 61 YRKEACGELTGTVCPCPGTYIAHLNLSKLCQCMCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEECQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
QY 241 VQRKQAEAGATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
DB 241 VQRKQAEAGATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 12

US-09-480-284-1
; Sequence 1, Application US/09480284
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi and Scot A. Marsters
; TITLE OF INVENTION: HIVM Polypeptides and Uses Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/480,284
; FILING DATE: 10-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/987,902
; FILING DATE: 10-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1068R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-480-284-1

Query Match 100.0%; Score 1578; DB 18; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPPGDGMPWRSPRTDVLRLVLYLFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
DB 1 MPPGDGMPWRSPRTDVLRLVLYLFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
QY 61 YRKEACGELTGTVCPCPGTYIAHLNLSKLCQCMCDPAMGLRASNCRSTENAVCG 120
DB 61 YRKEACGELTGTVCPCPGTYIAHLNLSKLCQCMCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEECQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
QY 241 VQRKQAEAGATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
DB 241 VQRKQAEAGATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEECQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
QY 241 VQRKQAEAGATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
DB 241 VQRKQAEAGATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 13

US-09-533-262-26
; Sequence 26, Application US/09533262
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Genetz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like 2
; FILE REFERENCE: 1488.077000A
; CURRENT APPLICATION NUMBER: US/09/533,262
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: US 60/147,383
; EARLIER FILING DATE: 1999-08-06
; EARLIER APPLICATION NUMBER: US 60/135,169
; EARLIER FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: US 60/126,522
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: US 60/125,683
; EARLIER FILING DATE: 1999-03-22
; EARLIER APPLICATION NUMBER: US 08/741,095
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/464,595
; EARLIER FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: US 08/462,962
; EARLIER FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: US 08/462,315
; EARLIER FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: PCT/US95/05058
; EARLIER FILING DATE: 1995-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-262-26

Query Match 100.0%; Score 1578; DB 19; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPPGDGMPWRSPRTDVLRLVLYLFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
DB 1 MPPGDGMPWRSPRTDVLRLVLYLFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
QY 61 YRKEACGELTGTVCPCPGTYIAHLNLSKLCQCMCDPAMGLRASNCRSTENAVCG 120
DB 61 YRKEACGELTGTVCPCPGTYIAHLNLSKLCQCMCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEECQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
QY 241 VQRKQAEAGATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
DB 241 VQRKQAEAGATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 14
US-09-791-537-41397
Sequence 41397, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 41397
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-41397
Query Match 100.0%; Score 1578; DB 22; Length 283;
Best Local Similarity 100.0%; Freq. No. 7,2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPPGDGPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDDEYVPSGCCPKCSPG 60
DB 1 MEPPGDGPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDDEYVPSGCCPKCSPG 60
QY 61 YRVKACGELTGVCCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGVCCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTVDDGHCACACRAVATSSPQKVGSTESQDTLQNCPPGTSPNGTLEECQ 180
DB 121 CSPGHFCTVDDGHCACACRAVATSSPQKVGSTESQDTLQNCPPGTSPNGTLEECQ 180
QY 181 HQTKCSMLVTKAGAGTSSSHMMWMLGSLVIVIVGCTVGLIICVKKRKRGGVVKVIYS 240
DB 181 HQTKCSMLVTKAGAGTSSSHMMWMLGSLVIVIVGCTVGLIICVKKRKRGGVVKVIYS 240
QY 241 VQKROEAGEGATVTEALQAPPDVTVAVEETIPSTFGSRPNH 283
DB 241 VQKROEAGEGATVTEALQAPPDVTVAVEETIPSTFGSRPNH 283

PRIOR FILING DATE: April 29, 1998
PRIOR APPLICATION NUMBER: 60/082,767
PRIOR FILING DATE: April 23, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/066,772
PRIOR FILING DATE: November 24, 1997
PRIOR APPLICATION NUMBER: 60/032,705
PRIOR FILING DATE: December 12, 1996
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: 09/709,238
PRIOR FILING DATE: November 8, 2000
PRIOR APPLICATION NUMBER: 09/664,610
PRIOR FILING DATE: September 18, 2000
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: September 18, 2000
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: August 23, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14941
PRIOR FILING DATE: May 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/13705
PRIOR FILING DATE: May 17, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05004
PRIOR FILING DATE: February 24, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: February 18, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04342
PRIOR FILING DATE: February 18, 2000
PRIOR APPLICATION NUMBER: 09/480,284
PRIOR FILING DATE: January 10, 2000
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: December 2, 1999
PRIOR APPLICATION NUMBER: 09/423,844
PRIOR FILING DATE: November 12, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: November 30, 1999
PRIOR APPLICATION NUMBER: 09/403,297
PRIOR FILING DATE: October 18, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: September 1, 1999
PRIOR APPLICATION NUMBER: 09/380,137
PRIOR FILING DATE: August 25, 1999
PRIOR APPLICATION NUMBER: 09/380,138
PRIOR FILING DATE: August 25, 1999
PRIOR APPLICATION NUMBER: 09/380,139
PRIOR FILING DATE: August 25, 1999
PRIOR APPLICATION NUMBER: 09/367,206
PRIOR FILING DATE: August 9, 1999
PRIOR APPLICATION NUMBER: 09/369,028
PRIOR FILING DATE: August 4, 1999

/ PRIOR APPLICATION NUMBER: PCT/US99/12252
/ PRIOR FILING DATE: June 2, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/08847
/ PRIOR FILING DATE: April 23, 1999
/ PRIOR APPLICATION NUMBER: 09/298,404
/ PRIOR FILING DATE: April 23, 1999
/ PRIOR APPLICATION NUMBER: 09/284,291
/ PRIOR FILING DATE: April 12, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/05028
/ PRIOR FILING DATE: March 8, 1999
/ PRIOR APPLICATION NUMBER: 09/254,311
/ PRIOR FILING DATE: March 3, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/00106
/ PRIOR FILING DATE: January 5, 1999
/ PRIOR APPLICATION NUMBER: 09/218,517
/ PRIOR FILING DATE: December 22, 1998
/ PRIOR APPLICATION NUMBER: 09/216,021
/ PRIOR FILING DATE: December 16, 1998
/ PRIOR APPLICATION NUMBER: PCT/US98/25108
/ PRIOR FILING DATE: December 1, 1998
/ PRIOR APPLICATION NUMBER: PCT/US98/19330
/ PRIOR FILING DATE: September 16, 1998
/ PRIOR APPLICATION NUMBER: 09/065,275
/ PRIOR FILING DATE: April 23, 1998
/ PRIOR APPLICATION NUMBER: 08/987,902
/ PRIOR FILING DATE: December 10, 1997
/ PRIOR APPLICATION NUMBER: PCT/US97/22278
/ PRIOR FILING DATE: December 5, 1997
/ NUMBER OF SEQ ID NOS: 113
/ SEQ ID NO 46
/ LENGTH: 283
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-882-636-46

Query Match 100.0%; Score 1578; DB 23; Length 283;
Best Local Similarity 100.0%; Pred. No. 7,2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPDGMGPPRSTPRTDVLRVLVLTFLGAPCYAPALPSCKEDEYVGSCECPKCSPG 60
DB 1 MEPPDGMGPPRSTPRTDVLRVLVLTFLGAPCYAPALPSCKEDEYVGSCECPKCSPG 60
QY 61 YRVKACGELTGTVCCEPCTGYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCCEPCTGYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPGTFSPNGTLEECQ 180
QY 181 HOTKCSWLVYTAGAGTSSSHWFWFLSGSLVIVYCVSTVGLIICVRRKPRGADVVKVIVS 240
DB 181 HOTKCSWLVYTAGAGTSSSHWFWFLSGSLVIVYCVSTVGLIICVRRKPRGADVVKVIVS 240
QY 241 VORKROEAGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283
DB 241 VORKROEAGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283

Search completed: November 14, 2003, 17:35:59
Job time : 176 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 17:30:56 ; Search time 20 Seconds
(without alignment)
683.668 Million cell updates/sec

Title: US-08-741-095B-26
Perfect score: 1578
Sequence: 1 MEBPGDWGPPMRSTPRTDY.....VTVAVEETIPSTGSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 255527 seqs, 48315734 residues

Total number of hits satisfying chosen parameters: 255527

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New.*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pcp.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pcp.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pcp.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pcp.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pcp.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pcp.*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1578	100.0	283	1 PCT-US02-29560A-288	Sequence 288, App
2	1575	99.8	283	6 US-10-322-281-546	Sequence 546, App
3	1575	99.8	283	6 US-10-322-281-548	Sequence 548, App
4	1575	99.8	283	6 US-10-322-281-550	Sequence 550, App
5	1575	99.8	283	7 US-60-512-690-303	Sequence 303, App
6	1575	99.8	283	7 US-60-512-690-304	Sequence 304, App
7	1575	99.8	283	7 US-60-512-690-305	Sequence 305, App
8	1575	99.8	283	7 US-60-512-690-306	Sequence 306, App
9	1477	93.6	282	1 PCT-US03-28227-3157	Sequence 3157, App
10	1477	93.6	282	1 PCT-US03-28227-3158	Sequence 3158, App
11	1477	93.6	282	1 PCT-US03-28227-3159	Sequence 3159, App
12	1477	93.6	282	1 PCT-US03-28227-3160	Sequence 3160, App
13	1477	93.6	282	1 PCT-US03-28227-3161	Sequence 3161, App
14	990	62.7	199	7 US-60-512-690-308	Sequence 308, App
15	990	62.7	199	7 US-60-512-690-307	Sequence 307, App
16	384.5	24.4	194	6 US-10-322-281-543	Sequence 543, App
17	267.5	17.0	277	1 PCT-US02-29560A-281	Sequence 281, App
18	267.5	17.0	277	1 PCT-US03-32827-28	Sequence 28, App1
19	267.5	17.0	277	5 US-09-467-317-2	Sequence 2, App1
20	267.5	17.0	277	6 US-10-688-845-28	Sequence 323, App
21	264.5	16.8	431	1 PCT-US03-28227-3226	Sequence 3226, App
22	259	16.4	182	4 US-08-484-783B-14	Sequence 14, App1
23	259	16.4	184	4 US-08-484-783B-15	Sequence 15, App1
24	259	16.4	235	4 US-08-484-783B-13	Sequence 13, App1
25	259	16.4	235	5 US-09-882-735A-16	Sequence 16, App1
26	259	16.4	235	5 US-09-882-735A-16	Sequence 16, App1

ALIGNMENTS

27	259	16.4	461	1 PCT-US03-31974-32	Sequence 32, App1
28	259	16.4	461	4 US-08-484-783B-12	Sequence 12, App1
29	259	16.4	461	6 US-10-456-819-17	Sequence 17, App1
30	259	16.4	461	7 US-60-487-610-2160	Sequence 2160, App
31	258.5	16.4	461	6 US-10-328-953-318	Sequence 318, App1
32	256	16.2	218	5 US-09-569-611C-33	Sequence 33, App1
33	256	16.2	218	5 US-09-569-611B-33	Sequence 33, App1
34	256	16.2	218	5 US-09-569-611C-33	Sequence 33, App1
35	253	16.0	435	1 PCT-US03-24669-353	Sequence 353, App
36	253	16.0	446	1 PCT-US03-28227-3859	Sequence 3859, App
37	253	16.0	450	1 PCT-US03-24669-354	Sequence 354, App
38	247.5	15.7	439	1 PCT-US03-28227-3860	Sequence 3860, App
39	246	15.6	300	1 PCT-US02-29560A-230	Sequence 230, App
40	246	15.6	300	1 PCT-US02-29560A-231	Sequence 231, App
41	246	15.6	300	6 US-10-456-819-1	Sequence 1, App1
42	240	15.2	399	1 PCT-US03-24669-352	Sequence 352, App
43	240	15.2	410	1 PCT-US03-28227-3861	Sequence 3861, App
44	240	15.2	635	1 PCT-US03-24669-355	Sequence 355, App
45	239	15.1	305	1 PCT-US03-24669-357	Sequence 357, App

RESULT 1
PCT-US02-29560A-288
Sequence 288, Application PC/TUS0229560A
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Gish, Kurt C.
APPLICANT: Hevez, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Wilson, Keith E.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-002710PC
CURRENT APPLICATION NUMBER: PCT/US02/29560A
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: US 60/323,469
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 412
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 288
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-29560A-288
Query Match 100.0%; Score 1578; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 4.8e-55;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MEBPGDWGPPMRSTPRTDYLVLTFLGAPCAVAPALPSCXEDYVPGSECCPCSPG 60
1 MEBPGDWGPPMRSTPRTDYLVLTFLGAPCAVAPALPSCXEDYVPGSECCPCSPG 60
61 YVKEACGELTGTVECPGTYIAHLNGLSKLOCOMDPAMGLASRNCRSTENAVCG 120
61 YVKEACGELTGTVECPGTYIAHLNGLSKLOCOMDPAMGLASRNCRSTENAVCG 120
61 YVKEACGELTGTVECPGTYIAHLNGLSKLOCOMDPAMGLASRNCRSTENAVCG 120
121 CSPGHFIVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTFSPNGTLEBO 180
121 CSPGHFIVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTFSPNGTLEBO 180
181 HQTCKSWLVTXKAGATSSSHWVFLSGSLVIVICSTYGLIICVRRKRGDVAVIYS 240
181 HQTCKSWLVTXKAGATSSSHWVFLSGSLVIVICSTYGLIICVRRKRGDVAVIYS 240
241 VQRKQEAEGEATVLEAQPDPVTVAVEETIPSTGSPNH 283
241 VQRKQEAEGEATVLEAQPDPVTVAVEETIPSTGSPNH 283

Db 241 VORKROEAGEATVIEALQAPPDVTTVAEETIPSTFGSRPNH 283

RESULT 2

US-10-322-281-546

; Sequence 546, Application US/10322281

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc S. Malandro

; TITLE OF INVENTION: Novel Compositions and Methods in Cancer

; FILE REFERENCE: 529452001000

; CURRENT APPLICATION NUMBER: US/10/322,281

; CURRENT FILING DATE: 2002-12-17

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 546

; LENGTH: 283

; TYPE: PRF

; ORGANISM: Homo sapiens

US-10-322-281-546

Query Match

Best Local Similarity 99.8%; Score 1575; DB 6; Length 283;

Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWRSTPRDVLRLVLYLTLFLGAPCAAPALPSCKEDEYVGSCECCPKCSFG 60

Db 1 MEPPGDMGPPWRSTPRDVLRLVLYLTLFLGAPCAAPALPSCKEDEYVGSCECCPKCSFG 60

QY 61 YRVKACGELTGTCVCEPPTGYIAHLNGLSKLCQCMCDPAMGLRASNCRSTENAVCG 120

Db 61 YRVKACGELTGTCVCEPPTGYIAHLNGLSKLCQCMCDPAMGLRASNCRSTENAVCG 120

QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESQDTLCNCPPTGSPNGTLEBQ 180

Db 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESQDTLCNCPPTGSPNGTLEBQ 180

QY 181 HOTKCSMLVTAKAGATSSSHWMMFLSGSLVIYVCSVGLIICVRRKPRGDVVKIVIS 240

Db 181 HOTKCSMLVTAKAGATSSSHWMMFLSGSLVIYVCSVGLIICVRRKPRGDVVKIVIS 240

QY 241 VORKROEAGEATVIEALQAPPDVTTVAEETIPSTFGSRPNH 283

Db 241 VORKROEAGEATVIEALQAPPDVTTVAEETIPSTFGSRPNH 283

RESULT 3

US-10-322-281-548

; Sequence 548, Application US/10322281

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc S. Malandro

; TITLE OF INVENTION: Novel Compositions and Methods in Cancer

; FILE REFERENCE: 529452001000

; CURRENT APPLICATION NUMBER: US/10/322,281

; CURRENT FILING DATE: 2002-12-17

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 548

; LENGTH: 283

; TYPE: PRF

; ORGANISM: Homo sapiens

US-10-322-281-548

Query Match

Best Local Similarity 99.8%; Score 1575; DB 6; Length 283;

Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWRSTPRDVLRLVLYLTLFLGAPCAAPALPSCKEDEYVGSCECCPKCSFG 60

Db 1 MEPPGDMGPPWRSTPRDVLRLVLYLTLFLGAPCAAPALPSCKEDEYVGSCECCPKCSFG 60

QY 61 YRVKACGELTGTCVCEPPTGYIAHLNGLSKLCQCMCDPAMGLRASNCRSTENAVCG 120

Db 61 YRVKACGELTGTCVCEPPTGYIAHLNGLSKLCQCMCDPAMGLRASNCRSTENAVCG 120

QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESQDTLCNCPPTGSPNGTLEBQ 180

Db 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESQDTLCNCPPTGSPNGTLEBQ 180

QY 181 HOTKCSMLVTAKAGATSSSHWMMFLSGSLVIYVCSVGLIICVRRKPRGDVVKIVIS 240

Db 181 HOTKCSMLVTAKAGATSSSHWMMFLSGSLVIYVCSVGLIICVRRKPRGDVVKIVIS 240

QY 241 VORKROEAGEATVIEALQAPPDVTTVAEETIPSTFGSRPNH 283

Db 241 VORKROEAGEATVIEALQAPPDVTTVAEETIPSTFGSRPNH 283

RESULT 4

US-10-322-281-550

; Sequence 550, Application US/10322281

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc S. Malandro

; TITLE OF INVENTION: Novel Compositions and Methods in Cancer

; FILE REFERENCE: 529452001000

; CURRENT APPLICATION NUMBER: US/10/322,281

; CURRENT FILING DATE: 2002-12-17

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 550

; LENGTH: 283

; TYPE: PRF

; ORGANISM: Homo sapiens

US-10-322-281-550

Query Match

Best Local Similarity 99.8%; Score 1575; DB 6; Length 283;

Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWRSTPRDVLRLVLYLTLFLGAPCAAPALPSCKEDEYVGSCECCPKCSFG 60

Db 1 MEPPGDMGPPWRSTPRDVLRLVLYLTLFLGAPCAAPALPSCKEDEYVGSCECCPKCSFG 60

QY 61 YRVKACGELTGTCVCEPPTGYIAHLNGLSKLCQCMCDPAMGLRASNCRSTENAVCG 120

Db 61 YRVKACGELTGTCVCEPPTGYIAHLNGLSKLCQCMCDPAMGLRASNCRSTENAVCG 120

QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESQDTLCNCPPTGSPNGTLEBQ 180

Db 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESQDTLCNCPPTGSPNGTLEBQ 180

QY 181 HOTKCSMLVTAKAGATSSSHWMMFLSGSLVIYVCSVGLIICVRRKPRGDVVKIVIS 240

Db 181 HOTKCSMLVTAKAGATSSSHWMMFLSGSLVIYVCSVGLIICVRRKPRGDVVKIVIS 240

QY 241 VORKROEAGEATVIEALQAPPDVTTVAEETIPSTFGSRPNH 283

Db 241 VORKROEAGEATVIEALQAPPDVTTVAEETIPSTFGSRPNH 283

RESULT 5

US-60-512-690-303

; Sequence 303, Application US/60512690

; GENERAL INFORMATION:

; APPLICANT: DOMON, Bruno

; APPLICANT: HE, Tao

; APPLICANT: LI, Aigun

; APPLICANT: ZHANG, Xiaolong

; APPLICANT: KETCHUM, Karen

; APPLICANT: MCCAFFERY, Ian

; APPLICANT: NARAYAN, Vaibhav

; TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES

; FILE REFERENCE: CLO01478PROV


```

; CURRENT APPLICATION NUMBER: US/60/512,690
; CURRENT FILING DATE: 2003-10-23
; NUMBER OF SEQ ID NOS: 1027
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 283
; TYPE: PRF
; ORGANISM: Homo sapiens
US-60-512-690-303
```

```

Query Match          99.8%; Score 1575; DB 7; Length 283;
Best Local Similarity 99.6%; Pred. No. 6.3e-55;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 MEBPGDWGPPPMRSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYVPGSECCPKCSPG 60
DB 1 MEBPGDWGPPPMRSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYVPGSECCPKCSPG 60
QY 61 YRVKACGELTGTVCBPCPGTYIAHLNGLSKLCQCOMDPAMGLRASNCSTRTENAAGC 120
DB 61 YRVKACGELTGTVCBPCPGTYIAHLNGLSKLCQCOMDPAMGLRASNCSTRTENAAGC 120
QY 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
DB 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKRGDVAVKIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKRGDVAVKIVS 240
QY 241 VOKRQEAEGEATVIEALQAPDVTTVAAVEETIPSTFGSPNH 283
DB 241 VOKRQEAEGEATVIEALQAPDVTTVAAVEETIPSTFGSPNH 283
```

```

RESULT 6
US-60-512-690-304
; Sequence 304, Application US/60512690
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno
; APPLICANT: HE, Tao
; APPLICANT: LI, Aiqun
; APPLICANT: ZHANG, Xiaolong
; APPLICANT: KETCHUM, Karen
; APPLICANT: MCCAFFERY, Ian
; APPLICANT: NARAYAN, Vaibhav
; TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES
; FILE REFERENCE: CL001478PROV
; CURRENT APPLICATION NUMBER: US/60/512,690
; CURRENT FILING DATE: 2003-10-23
; NUMBER OF SEQ ID NOS: 1027
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 304
; LENGTH: 283
; TYPE: PRF
; ORGANISM: Homo sapiens
US-60-512-690-304
```

```

Query Match          99.8%; Score 1575; DB 7; Length 283;
Best Local Similarity 99.6%; Pred. No. 6.3e-55;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

DB 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKRGDVAVKIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKRGDVAVKIVS 240
QY 241 VOKRQEAEGEATVIEALQAPDVTTVAAVEETIPSTFGSPNH 283
DB 241 VOKRQEAEGEATVIEALQAPDVTTVAAVEETIPSTFGSPNH 283
```

```

RESULT 7
US-60-512-690-305
; Sequence 305, Application US/60512690
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno
; APPLICANT: HE, Tao
; APPLICANT: LI, Aiqun
; APPLICANT: ZHANG, Xiaolong
; APPLICANT: KETCHUM, Karen
; APPLICANT: MCCAFFERY, Ian
; APPLICANT: NARAYAN, Vaibhav
; TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES
; FILE REFERENCE: CL001478PROV
; CURRENT APPLICATION NUMBER: US/60/512,690
; CURRENT FILING DATE: 2003-10-23
; NUMBER OF SEQ ID NOS: 1027
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 283
; TYPE: PRF
; ORGANISM: Homo sapiens
US-60-512-690-305
```

```

Query Match          99.8%; Score 1575; DB 7; Length 283;
Best Local Similarity 99.6%; Pred. No. 6.3e-55;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 MEBPGDWGPPPMRSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYVPGSECCPKCSPG 60
DB 1 MEBPGDWGPPPMRSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYVPGSECCPKCSPG 60
QY 61 YRVKACGELTGTVCBPCPGTYIAHLNGLSKLCQCOMDPAMGLRASNCSTRTENAAGC 120
DB 61 YRVKACGELTGTVCBPCPGTYIAHLNGLSKLCQCOMDPAMGLRASNCSTRTENAAGC 120
QY 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
DB 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKRGDVAVKIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKRGDVAVKIVS 240
QY 241 VOKRQEAEGEATVIEALQAPDVTTVAAVEETIPSTFGSPNH 283
DB 241 VOKRQEAEGEATVIEALQAPDVTTVAAVEETIPSTFGSPNH 283
```

```

RESULT 8
US-60-512-690-306
; Sequence 306, Application US/60512690
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno
; APPLICANT: HE, Tao
; APPLICANT: LI, Aiqun
; APPLICANT: ZHANG, Xiaolong
; APPLICANT: KETCHUM, Karen
; APPLICANT: MCCAFFERY, Ian
; APPLICANT: NARAYAN, Vaibhav
; TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES
; FILE REFERENCE: THEROOF
```



```
FILE REFERENCE: CL001478PROV
CURRENT APPLICATION NUMBER: US/60/512,690
CURRENT FILING DATE: 2003-10-23
NUMBER OF SEQ ID NOS: 1027
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 306
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-60-512-690-306

Query Match          99.8%; Score 1575; DB 7; Length 283;
Best Local Similarity 99.6%; Pred. No. 6,3e-55;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPGDWGPWPWRSTPRTDVLRVLVYLTFLGAPCAPALPSCKEDEYVPGSECCPKCSPG 60
DB 1 MPPGDWGPWPWRSTPRTDVLRVLVYLTFLGAPCAPALPSCKEDEYVPGSECCPKCSPG 60
QY 61 YVKEACGELTGTCCEPPTGTIAHLNGLSKLCLOQCDPAMGLRASRNCSTENAVCG 120
DB 61 YVKEACGELTGTCCEPPTGTIAHLNGLSKLCLOQCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSFNGTLEBQ 180
DB 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSFNGTLEBQ 180
QY 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVKKRRPRGADVVKIVS 240
DB 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVKKRRPRGADVVKIVS 240
QY 241 VQRRQEAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
DB 241 VQRRQEAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283

RESULT 9
PCT-US03-28227-3157
Sequence 3157, Application PC/TUS0328227
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
APPLICANT: HARTSHORNE, ToINETTE A.; SUCHOROLSKI, Martin;
APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
APPLICANT: DELEGANE, Angelo M.; PANESAR, Iqbal S.;
APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
APPLICANT: PANZER, Scott R.; WANG, Xinhao;
APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
APPLICANT: WU, Mingham C.; STUVE, Laura L.;
APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
APPLICANT: VITT, Ursula A.; KIRTON, Edward;
APPLICANT: KU, Yuning; KWONG, Mary;
APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
APPLICANT: MA, Yan; JACKSON, Jennifer L.;
APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PN-0100 PCT
CURRENT APPLICATION NUMBER: PCT/US03/28227
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/410,260
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/410,259
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 5444
SOFTWARE: PERL Program
SEQ ID NO 3157
```

```
LENGTH: 282
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 928524.PT115P
PCT-US03-28227-3157

Query Match          99.6%; Score 1477; DB 1; Length 282;
Best Local Similarity 99.2%; Pred. No. 3,8e-51;
Matches 263; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPPGDWGPWPWRSTPRTDVLRVLVYLTFLGAPCAPALPSCKEDEYVPGSECCPKCSPG 60
DB 1 MPPGDWGPWPWRSTPRTDVLRVLVYLTFLGAPCAPALPSCKEDEYVPGSECCPKCSPG 60
QY 61 YVKEACGELTGTCCEPPTGTIAHLNGLSKLCLOQCDPAMGLRASRNCSTENAVCG 120
DB 61 YVKEACGELTGTCCEPPTGTIAHLNGLSKLCLOQCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSFNGTLEBQ 180
DB 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSFNGTLEBQ 180
QY 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVKKRRPRGADVVKIVS 240
DB 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVKKRRPRGADVVKIVS 240
QY 241 VQRRQEAEGEATVIEALQAPPDVT 265
DB 241 VQRRQEAEGEATVIEALQAPPDAT 265

RESULT 10
PCT-US03-28227-3158
Sequence 3158, Application PC/TUS0328227
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
APPLICANT: HARTSHORNE, ToINETTE A.; SUCHOROLSKI, Martin;
APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
APPLICANT: DELEGANE, Angelo M.; PANESAR, Iqbal S.;
APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
APPLICANT: PANZER, Scott R.; WANG, Xinhao;
APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
APPLICANT: WU, Mingham C.; STUVE, Laura L.;
APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
APPLICANT: VITT, Ursula A.; KIRTON, Edward;
APPLICANT: KU, Yuning; KWONG, Mary;
APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
APPLICANT: MA, Yan; JACKSON, Jennifer L.;
APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PN-0100 PCT
CURRENT APPLICATION NUMBER: PCT/US03/28227
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/410,260
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/410,259
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 5444
SOFTWARE: PERL Program
SEQ ID NO 3158
TYPE: PRT
ORGANISM: Homo sapiens
```


FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 928524.PT117P
PCT-US03-28227-3158

Query Match 93.6%; Score 1477; DB 1; Length 282;
Best Local Similarity 99.2%; Pred. No. 3.8e-51;
Matches 263; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMPPMRSTPTDVLRLVLYLFLGAPCYALPSCKEDEYVSGCCPKSPG 60
DB 1 MEPPGDMPPMRSTPTDVLRLVLYLFLGAPCYALPSCKEDEYVSGCCPKSPG 60
QY 61 YRVKACGELTGYCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGYCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTVODGHCACRAVATSSPGQVOKGOTESODTLQNCPCPTGSPNGTLEECQ 180
DB 121 CSPGHFCTVODGHCACRAVATSSPGQVOKGOTESODTLQNCPCPTGSPNGTLEECQ 180
QY 181 HOTKCSWLTKAGAGTSSSHWMMFLSGSLVIYIVCSVGLIICVKRRKRGDVVKYIVS 240
DB 181 HOTKCSWLTKAGAGTSSSHWMMFLSGSLVIYIVCSVGLIICVKRRKRGDVVKYIVS 240
QY 241 VORRQAEAGEATVIEALQAPPDVT 265
DB 241 VORRQAEAGEATVIEALQAPPDVT 265

RESULT 11

PCT-US03-28227-3159
Sequence 3159, Application PC/TUS0328227

GENERAL INFORMATION:

APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
APPLICANT: HARTSHORNE, ToINETTE A.; SUCHOROLSKI, Martin;
APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
APPLICANT: DELEGANE, Angelo M.; PANESAR, Iqbal S.;
APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
APPLICANT: PANZER, Scott R.; WANG, Xinhao;
APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
APPLICANT: WU, Mingham C.; STUVE, Laura L.;
APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
APPLICANT: VITT, Ursula A.; KIRTON, Edward;
APPLICANT: XU, Yuming; KWONG, Mary;
APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
APPLICANT: MA, Yan; JACKSON, Jennifer L.;
APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PN-0100 PCT
CURRENT APPLICATION NUMBER: PCT/US03/28227
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/410,260
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/410,259
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 5444
SOFTWARE: PERL Program
SEQ ID NO 3159
LENGTH: 282
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 928524.PT130P

PCT-US03-28227-3159

Query Match 93.6%; Score 1477; DB 1; Length 282;
Best Local Similarity 99.2%; Pred. No. 3.8e-51;
Matches 263; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMPPMRSTPTDVLRLVLYLFLGAPCYALPSCKEDEYVSGCCPKSPG 60
DB 1 MEPPGDMPPMRSTPTDVLRLVLYLFLGAPCYALPSCKEDEYVSGCCPKSPG 60
QY 61 YRVKACGELTGYCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGYCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTVODGHCACRAVATSSPGQVOKGOTESODTLQNCPCPTGSPNGTLEECQ 180
DB 121 CSPGHFCTVODGHCACRAVATSSPGQVOKGOTESODTLQNCPCPTGSPNGTLEECQ 180
QY 181 HOTKCSWLTKAGAGTSSSHWMMFLSGSLVIYIVCSVGLIICVKRRKRGDVVKYIVS 240
DB 181 HOTKCSWLTKAGAGTSSSHWMMFLSGSLVIYIVCSVGLIICVKRRKRGDVVKYIVS 240
QY 241 VORRQAEAGEATVIEALQAPPDVT 265
DB 241 VORRQAEAGEATVIEALQAPPDVT 265

RESULT 12

PCT-US03-28227-3160
Sequence 3160, Application PC/TUS0328227

GENERAL INFORMATION:

APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
APPLICANT: HARTSHORNE, ToINETTE A.; SUCHOROLSKI, Martin;
APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
APPLICANT: DELEGANE, Angelo M.; PANESAR, Iqbal S.;
APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
APPLICANT: PANZER, Scott R.; WANG, Xinhao;
APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
APPLICANT: WU, Mingham C.; STUVE, Laura L.;
APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
APPLICANT: VITT, Ursula A.; KIRTON, Edward;
APPLICANT: XU, Yuming; KWONG, Mary;
APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
APPLICANT: MA, Yan; JACKSON, Jennifer L.;
APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PN-0100 PCT
CURRENT APPLICATION NUMBER: PCT/US03/28227
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/410,260
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/410,259
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 5444
SOFTWARE: PERL Program
SEQ ID NO 3160
LENGTH: 282
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 928524.PT139P
PCT-US03-28227-3160

Query Match 93.6%; Score 1477; DB 1; Length 282;

Best Local Similarity 99.2%; Pred. No. 3.8e-51;
Matches 263; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPPGDMGPPMRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEYVGSSECCPKCSFG 60
Db 1 MPPGDMGPPMRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEYVGSSECCPKCSFG 60
QY 61 YRKEACGELTGTVEPCPGTYIAHLNGLSKCLQCCMDPAMGLASRNCSTRTENAVCG 120
Db 61 YRKEACGELTGTVEPCPGTYIAHLNGLSKCLQCCMDPAMGLASRNCSTRTENAVCG 120
QY 121 CSFGHFCIVQDDHCAACRAVATSSPGQRVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
Db 121 CSFGHFCIVQDDHCAACRAVATSSPGQRVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
QY 181 HOTKCSWLTKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVRRKPRGDVVKIVIS 240
Db 181 HOTKCSWLTKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVRRKPRGDVVKIVIS 240
QY 241 VORROEAGEATVIEALQAPPDVT 265
Db 241 VORROEAGEATVIEALQAPPDVT 265

RESULT 13

PCT-US03-28227-3161
Sequence 3161, Application PC/TUS0328227

GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION, SCHMIDT, Jeanette P.;
APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
APPLICANT: HARTSHORNE, ToINETTE A.; SUCHOROLSKI, Martin;
APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
APPLICANT: DELESPAN, Angelo M.; PANESAR, Iqbal S.;
APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
APPLICANT: PANZER, Scott R.; WANG, Xinhao;
APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
APPLICANT: WU, Mingham C.; STUVE, Laura L.;
APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
APPLICANT: VITT, Ursula A.; KIRTON, Edward;
APPLICANT: XU, Yuming; KWONG, Mary;
APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
APPLICANT: MA, Yan; JACKSON, Jennifer L.;
APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.;
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PR-0100 PCT
CURRENT APPLICATION NUMBER: PCT/US03/28227
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/410,260
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/410,259
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 5444
SOFTWARE: PERL Program
SEO ID NO 3161
LENGTH: 282
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 928524.PT146p
PCT-US03-28227-3161

Query Match 93.6%; Score 1477; DB 1; Length 282;
Best Local Similarity 99.2%; Pred. No. 3.8e-51;
Matches 263; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPPGDMGPPMRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEYVGSSECCPKCSFG 60
Db 1 MPPGDMGPPMRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEYVGSSECCPKCSFG 60

QY 61 YRKEACGELTGTVEPCPGTYIAHLNGLSKCLQCCMDPAMGLASRNCSTRTENAVCG 120
Db 61 YRKEACGELTGTVEPCPGTYIAHLNGLSKCLQCCMDPAMGLASRNCSTRTENAVCG 120

QY 121 CSFGHFCIVQDDHCAACRAVATSSPGQRVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
Db 121 CSFGHFCIVQDDHCAACRAVATSSPGQRVQKGTESODTLQNCPPGTFSPNGTLEBQ 180

QY 181 HOTKCSWLTKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVRRKPRGDVVKIVIS 240
Db 181 HOTKCSWLTKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVRRKPRGDVVKIVIS 240

QY 241 VORROEAGEATVIEALQAPPDVT 265
Db 241 VORROEAGEATVIEALQAPPDVT 265

RESULT 14

US-60-512-690-308
Sequence 308, Application US/60512690

GENERAL INFORMATION:
APPLICANT: DOMON, Bruno
APPLICANT: HE, Tao
APPLICANT: LI, Aigun
APPLICANT: ZHANG, Xiaolong
APPLICANT: KETCHUM, Karen
APPLICANT: MCCAFFERY, Ian
APPLICANT: NARAYAN, Vaibhav
TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES
FILE REFERENCE: CL001478PROV
CURRENT APPLICATION NUMBER: US/60/512,690
CURRENT FILING DATE: 2003-10-23
NUMBER OF SEQ ID NOS: 1027
SOFTWARE: FastSeq for Windows Version 4.0
SEO ID NO 308
LENGTH: 199
TYPE: PRT
ORGANISM: Homo sapiens
US-60-512-690-308

Query Match 62.7%; Score 990; DB 7; Length 199;
Best Local Similarity 100.0%; Pred. No. 2e-32;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 PAMGLASRNCSTRTENAVCGSPGHFCIVQDDHCAACRAVATSSPGQRVQKGTESODT 160

Db 17 PAMGLASRNCSTRTENAVCGSPGHFCIVQDDHCAACRAVATSSPGQRVQKGTESODT 76

QY 161 LQNCPPGTFSPNGTLEBQCHQTKCSWLTKAGAGTSSSHWWMFLSGSLVIVICSTVG 220

Db 77 LQNCPPGTFSPNGTLEBQCHQTKCSWLTKAGAGTSSSHWWMFLSGSLVIVICSTVG 136

QY 221 LIIICVRRKPRGDVVKIVISVORROEAGEATVIEALQAPPDVTVAEETIPFTGSR 280

Db 137 LIIICVRRKPRGDVVKIVISVORROEAGEATVIEALQAPPDVTVAEETIPFTGSR 196

QY 281 PNH 283

Db 197 PNH 199

RESULT 15

US-60-512-690-307
Sequence 307, Application US/60512690

GENERAL INFORMATION:
APPLICANT: DOMON, Bruno
APPLICANT: HE, Tao
APPLICANT: LI, Aigun


```

1  APPLICANT: ZHANG, Xiaolong
2  APPLICANT: KETCHUM, Karen
3  APPLICANT: MCCAFFERY, Ian
4  APPLICANT: NARAYAN, Vaibhav
5  TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USBS
6  TITLE OF INVENTION: THEREOF
7  FILE REFERENCE: CL001478PROV
8  CURRENT APPLICATION NUMBER: US/60/512,690
9  CURRENT FILING DATE: 2003-10-23
10 NUMBER OF SEQ ID NOS: 1027
11 SOFTWARE: FastSeq for Windows Version 4.0
12 SEQ ID NO 307
13 LENGTH: 172
14 TYPE: PRF
15 ORGANISM: Homo sapiens
16 US-60-512-690-307

```

Query Match	49.9%	Score 787	DB 7	Length 172
Best Local Similarity	99.3%	Pred	No. 1.2e-24	
Matches 143, Conservative	0	Mismatches 1	Indels 0	Gaps 0

Oy	101 PAMG,RASNGC RTEAAVCGSGHGC IYQDGHCAACRAVAATSPGORXOKGTSSODT 160
Dd	17 PAMGRASNGCRTEAANAVCGSCBPHCC IYQDGHCAACRAVAATSPGORXOKGTSSODT 76
Oy	161 LCONPPTGFSPNGTLPECOHOHKFCMLVTYKAGATSSSHWVMFLSGSLVIIVESTVG 220
Dd	77 LCQNPPPTGFSPNGTLPECOHOTKSMVLTKAGATSSSHWVMFLSGSLVIIVESTVG 136
Oy	221 LIICVRRRRPRGDVVKEIVSVORK 244
Dd	137 LIICVRRRRPRGDVVKEIVSVQAOK 160

Search completed: November 14, 2003, 17:36:32
Job time : 21 secs

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09/340690
N

27. (Once Amended) An isolated Human Tumor Necrosis Factor Receptor-Like 2 protein comprising amino acids 1 to 245 of SEQ ID NO:26.
28. The isolated protein of claim 27, which comprises amino acids -38 to 245 of SEQ ID NO:26.
29. The isolated protein of claim 27, which is produced by a recombinant host cell.
30. The isolated protein of claim 27, which comprises a heterologous polypeptide.
31. The isolated protein of claim 30, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.
32. (amended) A composition comprising the isolated protein of claim 27 and a carrier.
33. (amended) An isolated protein comprising 30 contiguous amino acids of the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97059, wherein said 30 contiguous amino acids comprises an antigenic determinant for the polypeptide consisting of the amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97059.
34. The isolated protein of claim 33, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97059.
35. The isolated protein of claim 33, which is produced by a recombinant host cell.
36. The isolated protein of claim 33, which comprises a heterologous polypeptide.
37. The isolated protein of claim 36, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.
38. (amended) A composition comprising the isolated protein of claim 33 and carrier.
45. (Once Amended) An isolated Human Tumor Necrosis Factor Receptor-Like protein comprising the mature amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97058.
46. The isolated protein of claim 45, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97058.
47. The isolated protein of claim 45, which is produced by a recombinant host cell.
48. The isolated protein of claim 45, which comprises a heterologous polypeptide.
49. The isolated protein of claim 48, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.
50. (amended) A composition comprising the isolated protein of claim 45 and a carrier.
57. (Once Amended) An isolated Human Tumor Necrosis Factor Receptor-Like protein comprising the mature amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057.

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58. The isolated protein of claim 57, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057.

59. The isolated protein of claim 57, which is produced by a recombinant host cell.

60. The isolated protein of claim 57, which comprises a heterologous polypeptide.

61. The isolated protein of claim 60, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

62. (amended) A composition comprising the isolated protein of claim 57 and a carrier.

81. (Once Amended) An isolated Human Tumor Necrosis Factor Receptor-Like 2 protein comprising amino acids 1 to 162 of SEQ ID NO:26.

82. The isolated protein of claim 81, which comprises amino acids -38 to 162 of

SEQ ID NO:26.

83. The isolated protein of claim 81, which is produced by a recombinant host cell.

84. The isolated protein of claim 81, which comprises a heterologous polypeptide.

85. The isolated protein of claim 84, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

86. (amended) A composition comprising the isolated protein of claim 81 and a

175. (new) An isolated protein comprising 30 contiguous amino acids of the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97058, wherein said 30 contiguous amino acids comprises an antigenic determinant or the polypeptide consisting of the amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97058.

176. (new) The isolated protein of claim 175, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97058.

177. (new) The isolated protein of claim 175, which is produced by a recombinant host cell.

178. (new) The isolated protein of claim 175, which comprises a heterologous polypeptide.

179. (new) The isolated protein of claim 178, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

180. (new) A composition comprising the isolated protein of claim 175 and a carrier.

carrier.

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complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057, wherein said 30 contiguous amino acids comprises an antigenic determinant or the polypeptide consisting of the amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057.

182. (new) The isolated protein of claim 181, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057.

183. (new) The isolated protein of claim 181, which is produced by a recombinant host cell.

184. (new) The isolated protein of claim 181, which comprises a heterologous polypeptide.

185. (new) The isolated protein of claim 184, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

186. (new) A composition comprising the isolated protein of claim 181 and a carrier.

polypeptide consisting of the amino acid sequence of SEQ ID NO: 26, wherein said 30 contiguous amino acids comprises an antigenic determinant for the polypeptide consisting of the amino acid sequence of SEQ ID NO: 26.

188. (new) The isolated protein of claim 187, which is produced by a recombinant host cell.

189. (new) The isolated protein of claim 187, which comprises a heterologous polypeptide.

190. (new) The isolated protein of claim 189, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

191. (new) A composition comprising the isolated protein of claim 187 and a carrier.

192. (new) An isolated protein comprising the mature amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97059.

193. (new) The isolated protein of claim 192, which is produced by a recombinant host cell.

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194. (new) The isolated protein of claim 192, which comprises a heterologous polypeptide.

195. (new) The isolated protein of claim 194, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

196. (new) A composition comprising the isolated protein of claim 192 and a carrier.

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41. (amended) An isolated antibody which specifically binds to a polypeptide consisting of amino acids -38 to 245 of SEQ ID No. 26. 09/533262 Ni

42. (Once amended) The isolated antibody of claim 41, wherein said antibody is monoclonal antibody.

43. (Once amended) The isolated antibody of claim 41, wherein said antibody is polyclonal antibody.

44. (Once amended) The isolated antibody of claim 41, wherein said antibody is chimeric antibody.

45. (Once amended) The isolated antibody of claim 41, wherein said antibody is humanized antibody.

46. (Once amended) The isolated antibody of claim 41, wherein said antibody is single-chain Fv antibody.

47. (Once amended) The isolated antibody of claim 41, wherein said antibody is Fab antibody fragment.

A composition comprising the Ab of claim 41 and a pharmaceutically acceptable carrier.

60. (New) The isolated antibody of claim 41, wherein said antibody is the product of an Fab expression library.

61. (amended) A method of producing the isolated antibody of claim 41, comprising immunizing an animal with a polypeptide comprising amino acids -38 to 245 of SEQ ID No.

and recovering an antibody, which specifically binds, said polypeptide.

62. (New) A hybridoma which produces the monoclonal antibody of claim 42.

63. (New) A method of producing a monoclonal antibody which comprises:
(a) culturing the hybridoma of claim 62 under appropriate conditions; and

(b) isolating monoclonal antibody therefrom.

64. (amended) An isolated antibody which specifically binds to a polypeptide consisting of amino acids -38 to 162 of SEQ ID No. 26.

65. (New) The isolated antibody of claim 64, wherein said antibody is a monoclonal antibody.

66. (New) The isolated antibody of claim 64, wherein said antibody is a polyclonal antibody.

67. (New) The isolated antibody of claim 64, wherein said antibody is a chimeric antibody.

68. (New) The isolated antibody of claim 64, wherein said antibody is a humanized antibody.

69. (New) The isolated antibody of claim 64, wherein said antibody is a single-chain Fv antibody.

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100. (amended) An isolated polynucleotide comprising a nucleic acid encoding a polypeptide comprising an amino acid sequence at least 90% identical to amino acids 1 to 162 of SEQ ID NO: 26, wherein said polypeptide inhibits T cell proliferation.

187. The polynucleotide of claim 186, wherein the sequence of said amino acid sequence is at least 90% identical to amino acids -38 to 162 of SEQ ID NO:26.

188. A method of producing a vector which comprises inserting the polynucleotide of claim 186 into a vector.

189. A vector comprising the polynucleotide of claim 186.

190. A host cell comprising the polynucleotide of claim 186 operably associated with a heterologous regulatory element.

191. A method of producing a polypeptide which comprises culturing the host cell of claim 190 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

192. (amended) An isolated polynucleotide comprising a nucleic acid encoding a polypeptide comprising an amino acid sequence at least 95% identical to amino acids 1 to 162 of SEQ ID NO: 26, wherein said polypeptide inhibits T cell proliferation.

193. The polynucleotide of claim 192, wherein the sequence of said amino acid sequence is at least 95% identical to amino acids -38 to 162 of SEQ ID NO:26.

194. A method of producing a vector which comprises inserting the polynucleotide of claim 192 into a vector.

195. A vector comprising the polynucleotide of claim 192.

196. A host cell comprising the polynucleotide of claim 192 operably associated with a heterologous regulatory element.

197. A method of producing a polypeptide which comprises culturing the host cell of claim 196 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

198. An isolated polynucleotide comprising a nucleic acid encoding amino acids 1 to 162 of SEQ ID NO:26.

199. The polynucleotide of claim 198, comprising nucleotides 123 to 608 of SEQ ID NO:25.

200. The polynucleotide of claim 198, comprising a nucleic acid encoding amino acids -38 to 162 of SEQ ID NO:26.

201. The polynucleotide of claim 200, comprising nucleotides 9 to 608 of SEQ ID NO:25.

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84. (New) A composition comprising the antibody of claim 76 and a pharmaceutically acceptable carrier.

85. (amended) A method of producing the isolated antibody of claim 76, comprising:
(a) immunizing an animal with a polypeptide comprising amino acids 1 to 162 of SEQ ID No. 26; and

(b) recovering an antibody, which specifically binds, said polypeptide.

86. (New) A hybridoma which produces the monoclonal antibody of claim 77.

87. (New) A method of producing a monoclonal antibody which comprises:
(a) culturing the hybridoma of claim 86 under appropriate conditions; and

(b) isolating monoclonal antibody therefrom.

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70. (New) The isolated antibody of claim 64, wherein said antibody is an Fab antibody fragment.

71. (New) The isolated antibody of claim 64, wherein said antibody is the product of an Fab expression library.

72. (New) A composition comprising the antibody of claim 64 and a pharmaceutically acceptable carrier.

73. (amended) A method of producing the isolated antibody of claim 64, comprising:

(a) immunizing an animal with a polypeptide comprising amino acids -38 to 162 of SEQ ID No. 26; and

(b) recovering an antibody which specifically binds said polypeptide.

74. (New) A hybridoma which produces the monoclonal antibody of claim 65.

75. (New) A method of producing a monoclonal antibody which comprises:

(a) culturing the hybridoma of claim 74 under appropriate conditions; and

(b) isolating monoclonal antibody therefrom.

77. (New) The isolated antibody of claim 76, wherein said antibody is a monoclonal antibody.

78. (New) The isolated antibody of claim 76, wherein said antibody is a polyclonal antibody.

79. (New) The isolated antibody of claim 76, wherein said antibody is a chimeric antibody.

80. (New) The isolated antibody of claim 76, wherein said antibody is a humanized antibody.

81. (New) The isolated antibody of claim 76, wherein said antibody is a single-chain Fv antibody.

82. (New) The isolated antibody of claim 76, wherein said antibody is an Fab antibody fragment.

83. (New) The isolated antibody of claim 76, wherein said antibody is the product of an Fab expression library.

consisting of amino acids 1 to 162 of SEQ ID No. 26.

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202. A method of producing a vector which comprises inserting the polynucleotide of claim 198 into a vector.

203. A vector comprising the polynucleotide of claim 198.

204. A host cell comprising the polynucleotide of claim 198 operably associated with a heterologous regulatory element.

205. A method of producing a polypeptide which comprises culturing the host cell of claim 204 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

206. (amended) An isolated polynucleotide comprising a nucleic acid encoding a polypeptide comprising an amino acid sequence at least 90% identical to amino acids 1 to 245 of SEQ ID NO: 26, wherein said polypeptide stimulates T cell proliferation.

207. The polynucleotide of claim 206, wherein the sequence of said amino acid sequence is at least 90% identical to amino acids -38 to 245 of SEQ ID NO:26.

208. A method of producing a vector which comprises inserting the polynucleotide of claim 206 into a vector.

209. A vector comprising the polynucleotide of claim 206.

210. A host cell comprising the polynucleotide of claim 206 operably associated with a heterologous regulatory element.

211. A method of producing a polypeptide which comprises culturing the host cell of claim 210 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

212. (amended) An isolated polynucleotide comprising a nucleic acid encoding a polypeptide comprising an amino acid sequence at least 95% identical to amino acids 1 to 245 of SEQ ID NO: 26, wherein said polypeptide stimulates T cell proliferation.

213. The polynucleotide of claim 212, wherein the sequence of said amino acid sequence is at least 95% identical to amino acids -38 to 245 of SEQ ID NO:26.

214. A method of producing a vector which comprises inserting the polynucleotide of claim 212 into a vector.

215. A vector comprising the polynucleotide of claim 212.

216. A host cell comprising the polynucleotide of claim 212 operably associated with a heterologous regulatory element.

217. A method of producing a polypeptide which comprises culturing the host cell of claim 216 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

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218. An isolated polynucleotide comprising a nucleic acid encoding amino acids 1 to 245 of SEQ ID NO:26.

219. The polynucleotide of claim 218, comprising nucleotides 123 to 857 of SEQ ID NO:25.

220. The polynucleotide of claim 218, comprising a nucleic acid encoding amino acids -38 to 245 of SEQ ID NO:26.

221. The polynucleotide of claim 220, comprising nucleotides 9 to 857 of SEQ ID NO:25.

222. A method of producing a vector which comprises inserting the polynucleotide of claim 218 into a vector.

223. A vector comprising the polynucleotide of claim 218.

224. A host cell comprising the polynucleotide of claim 218 operably associated with a heterologous regulatory element.

225. A method of producing a polypeptide which comprises culturing the host cell of claim 224 under conditions such that said polypeptide is expressed, and recovering said polypeptide.--

226. (new) An isolated polynucleotide comprising a nucleic acid encoding a polypeptide comprising 30 contiguous amino acids of the amino acid sequence of SE ID NO: 26, wherein said 30 contiguous amino acids comprises an antigenic determinant for the polypeptide consisting of the amino acid sequence of SEQ ID NO: 26.

227. (new) A method of producing a vector which comprises inserting the polynucleotide of claim 226 into a vector.

228. (new) A vector comprising the polynucleotide of claim 226.

229. (new) A host cell comprising the polynucleotide of claim 226 operably associated with a heterologous regulatory element.

230. (new) A method of producing a polypeptide which comprises culturing the host cell of claim 229 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

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